

## SEQUENCE LISTING

10/573600

<110> The Trustees of the University of Pennsylvania  
 Wilson, James M.  
 Gao, Guangping  
 Alvira, Mauricio R.  
 Vandenbergh, Luk H.

<120> Adeno-Associated Virus (AAV) Clades, Sequences, Vectors  
 Containing Same, and Uses Therefor

10/573600  
 20 MAR 2005

<130> UPN-P3230PCT

<150> US 60/508,226

<151> 2003-09-30

<150> US 60/566,546

<151> 2004-04-29

<160> 236

<170> PatentIn version 3.3

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<213> adeno-associated virus, clone hu.31

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 <213> adeno-associated virus, human clone 9

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attcagtaca cttcaaaact ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg ccccatgggt actcgttacc tcaccgtaa tctgtaa 2217

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<210> 7
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.38

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<400> 7
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gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aaggggggag ccgtcaacgc ggcggacgca gcggccctcg agcacgaca ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc caggggcatc 480
ggcaagaagc gccagcggcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
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atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840
ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900
cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gcccttcaac 960

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atccagggtca aggagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020
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caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
cttactactga acaatggaag tcaagccgta ggccgttcct ctttctactg cctggaatat 1200
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gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
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gtgtgtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
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ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
gtcagcgtgg aaatcgagt ggagctgcag aaggagaaca gcaaacgctg gaaccagag 2100
attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
ggaacttatt ctgagcctcg cccattggg actcgctacc tcaccgtaa tctgtaa 2217

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<210> 8
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.42

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<400> 8
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgagggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttcag 360
gccaagaagc ggggtctcga acctctcggg ctggttgagg aagcggctaa gacggctcct 420
ggaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggccctc tggctctggga 600
tctgggtacaa tggctgcagg cgggtggcgt ccaatggcag acaataacga aggcgccgac 660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
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cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
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caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
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tttccatctc aaatgctgcy aactggaaac aattttgaat tcagctacac cttcgaggac 1260

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gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320
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cagcaattgt tatttttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440
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agcaactttg cttggactgg tgccaccaa taccacctga acggaagaga ctctttggta 1560
aatccccgtg tcgccatggc aaccacaag gacgacgagg aacgcttctt cccgtcgagt 1620
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gtgggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggccccatc 1860
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ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040
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attcagtaca cttcaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160
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<210> 9
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.72

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```

<400> 9
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctgggtct tcctgggtac aagtacctg gaccttcaa cggactcgac 180
aaggggggagc ccgtcaacgc ggcggacgca gcgccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtctagtc ccgacctca accaatcgga gaaccaccag caggccccctc tggctcggga 600
tctggtacaa tggtcgcagg cgggtggcgt ccaatggcag acaataacga aggcgcccag 660
ggagtgggta gttcctcagg aaattggcat tgcgattcca catgggtggg cgacagagtc 720
atcaccacca gacccgaac ctgggccctg cccacctaca acaaccact ctacaagcaa 780
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cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
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caccagggtc gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140
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cagcaattgt tatttttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440
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aatccccggtg tcgccatggc aaccacacaag gacgacgagg aacgcttctt cccgtcgagt 1620
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atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggg 1740
gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800
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attcagtaca cttcaaaact ctacaaatct acaaattgtg actttgctgt caatacagag 2160
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<210> 10
<211> 2217
<212> DNA
<213> new AAV serotype, clone hu.37

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<400> 10
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagac gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480
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gagtcagtc ccgaccctca accaatcgga gaaccaccag caggccctc tggctcggga 600
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ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
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cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960
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attcagtaca cttcaaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag	2160
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<210> 11  
 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone hu.40

<400> 11	
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gacggccggg gtctgggtgt tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aagggggagc ccgtcaacgc ggcgagcgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aagcgggtga caatccgtac ctgagggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
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attcagtaca cttcaaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag	2160

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 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone hu.38

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 gacggccggg gtctgggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac 240  
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 gccaaagac gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480  
 ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540  
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 tctggtacaa tggctgcagg cgggtgcgct ccaatggcag acaataacga aggcgccgac 660  
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 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960  
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 cttacactga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200  
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<210> 13  
 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.39  
 <400> 13

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 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.40

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&lt;210&gt; 15

&lt;211&gt; 2217

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone rh.64

&lt;400&gt; 15

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 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.68

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<210> 17
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.53

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<210> 18
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.52

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 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.46

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 <212> DNA  
 <213> new AAV serotype, clone rh.70

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<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.61

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<210> 22
<211> 2217
<212> DNA
<213> new AAV serotype, clone rh.51

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&lt;210&gt; 23

&lt;211&gt; 2217

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone rh.50

&lt;400&gt; 23

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 <212> DNA  
 <213> new AAV serotype, clone hu.39

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 <212> DNA  
 <213> new AAV serotype, clone rh.49

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 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.57

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&lt;210&gt; 27

&lt;211&gt; 2217

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone rh.58

&lt;400&gt; 27

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<210> 28
<211> 2196
<212> DNA
<213> new AAV serotype, clone pi.1

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<210> 29
<211> 2196
<212> DNA
<213> new AAV serotype, clone pi.3

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aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040
gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

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tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag cgaaccccg 2160  
cccattggca ctcgttacct caccgtaat ctgtaa 2196

<210> 30  
<211> 2196  
<212> DNA  
<213> new AAV serotype, clone pi.2

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gacggccggg gtctgggtgt tcttggttac aagtacctcg gacccttcaa cggactcgac 180  
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cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540  
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cccattggca ctcgttacct caccgtaat ctgtaa 2196

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<211> 2208  
<212> DNA  
<213> new AAV serotype, clone rh.60

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 acctcaatt ttgacaaaca gactggtgtg gactttgccg ttgacagcca ggggtgttat 2160  
 tctgagcctc gccccattgg tactcgttac ctacccgta atctgtaa 2208

<210> 32  
 <211> 2214  
 <212> DNA  
 <213> new AAV serotype, clone rh.48

<400> 32  
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 gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240



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 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480  
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 atcaccacca gcaaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780  
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<210> 33  
 <211> 2214  
 <212> DNA  
 <213> new AAV serotype, clone rh.62

<400> 33  
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 gacggccggg gtctgggtgt tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
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 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480  
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

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ggagtggtgta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840
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<210> 34  
 <211> 2214  
 <212> DNA  
 <213> new AAV serotype, clone rh.44

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<400> 34
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgaca ggcctgcgac 240
cagcggctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360
gccaaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactctc caggggcatc 480
ggcaagaag gccagcagc cgctagaaag agactgaact ttgggcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcggg gaaccaccag caggccccctc tggctctggga 600
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ggagtggtgta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcaccacca gcacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa 780
atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

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<210> 35
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.65

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aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
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cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160
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<210> 36
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.67

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gagtggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctc agcacgaca ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accatgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag 360
gccaagaagc gggttctcga acctctcgg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggcttgga 600
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cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

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cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160
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<210> 37
<211> 2214
<212> DNA
<213> new AAV serotype, clone rh.55

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gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgaca ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
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ggaaagaaga gaccggtaga gccgtacca cagcgttccc ccgactctc cacgggcatc 480
ggcaagaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540
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tctggtacaa tggtgcagg cgggtggcga ccaatggcag acaataacga aggtgccgac 660
ggagtgggta gttcctcggg aaattggcat tgcgattcca cacggctggg cgacagagtc 720
atcaccacca gcaccggac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780
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<210> 38  
 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.47

<400> 38  
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 gacggccggg gtctggtgct tcctggctac aagcacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
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 gccaaagaac gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactctc cacgggcatc 480  
 ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540  
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 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
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 atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840  
 ccctgggggt attttgactt taacagattc cactgccact tctcaccagc tgactggcag 900  
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960  
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 ccggagggtgt ttacgcctgc caagtttgct tctttcatca cacagtacag caccggccag 2040

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<210> 39  
 <211> 2214  
 <212> DNA  
 <213> new AAV serotype, clone rh.69

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 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180  
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 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccaaagaagc gggttctcga acctctcgggt ctggttgagg aagctgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480  
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 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840  
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 ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960  
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 ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860  
 gccaaagatt ctacacaga tggcaacttt caccctctc ctttaatggg cggttttgga 1920  
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 cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgaggg 2160  
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<210> 40  
 <211> 2214  
 <212> DNA

<213> new AAV serotype, clone rh.54

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 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
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 gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420  
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<210> 41  
 <211> 2214  
 <212> DNA  
 <213> new AAV serotype, clone rh.45

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 gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240



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 gccaaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420  
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 gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccctc tggctctggga 600  
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 atcaccacca gcaccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780  
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 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900  
 ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960  
 caggtaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020  
 acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080  
 cagggtgctc tgctccggt cccggcgagc gtcttcatga ttcctcagta cggctacctg 1140  
 actctcaaca acggtagtca ggcgtggga cgttctctct tctactgcct ggagtacttc 1200  
 cctctcaga tgctgagaac gggcaacaac ttttccttca gctacacttt cgaggacgtg 1260  
 cctttccaca gcagctacgc gcacagccag agtttgga ggcgtatgaa tcctctcatc 1320  
 gaccagtacc tgtactacct gtcaagaacc cagtctacgg gaggcacagc gggaaccag 1380  
 cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg 1440  
 cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc 1500  
 aactttgcct ggactggtgc caccaagtat catctgaacg gcagagactc tctggtgaat 1560  
 ccgggcgtcg ccatggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc 1620  
 atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg 1680  
 ctaaccagcg aggaagaaat caagaccacc aaccccgtag ccacagaaca gtatggcgtg 1740  
 gtggctgata acctacagca gcaaaacacc gctcctattg tgggggcccgt caacagccag 1800  
 ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg 1860  
 gccaaagattc ctacacaga tggcaacttt caccgtctc ctttaatggg cggttttggga 1920  
 cttaaacatc cgcctcctca gatccttacc aaaaacactc ctgttcctgc ggatcctcca 1980  
 acagcgttca accaggccaa gctgaattct ttcacacgc agtacagcac cggacaagtc 2040  
 agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgtggaa cccagagatt 2100  
 cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgaggg 2160  
 gcttactctg agcctcgccc cattggcact cgttacctca cccgtaactc gtaa 2214

<210> 42  
 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone rh.59

<400> 42  
 atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60  
 gagtgggtggg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120  
 gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcgagcgc gcgccctcg agcacgacaa ggcctacgac 240  
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccaaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcac 480  
 ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcggga gaaccaccag caggcccttc tggctctggga 600  
 tcttggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660  
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
 atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780  
 atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccctc 840  
 tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900  
 ctcatacaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960  
 cagggtcaagg aggtcacaaac gaatgacggc gtcacgacca tcgccaataa ccctaccagc 1020  
 acggttcagg tcttttcgga ctcggaatac cagctgcctt acgtcctcgg ctccgcacac 1080  
 cagggtgccc tgcctccgtt cccggcgagc gtcttcatga ttccccagta cggctacctg 1140  
 actctgaaca atggcagcca atcggtgggg cgcttctctt tctactgcct ggaatatctt 1200  
 ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260  
 cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320  
 gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380  
 cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440  
 ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500  
 agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctgggtg 1560  
 aatccgggagc tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620  
 ggcattctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680  
 atgctaacca gcgaggaaga aatcaagacc accaaccctg tggccacaga acagtatggc 1740  
 gtggtggctg ataacctaca gcagcaaac accgctccta ttgtgggggc cgtcaacagc 1800  
 caggggagcct tacctggcat ggtctggcag aaccgggagc tgtacctgca gggctctatt 1860  
 tggggccaaga ttcttcacac agatggcaac ttaccacctg ctcttctaag gggcggtctt 1920  
 ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctctgttcc tgcggatcct 1980  
 ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgagctacag caccggacaa 2040  
 gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgtg gaaccagag 2100  
 attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160  
 ggtgtttact ctgagcctcg cccattggc actcgttacc tcaccgtaa tctgtaa 2217

<210> 43  
 <211> 2211  
 <212> DNA  
 <213> new AAV serotype, clone rh.43

<400> 43  
 atggctgccc atggttatct tccagattgg ctgaggaca acctctctga gggcattcgc 60  
 gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120  
 gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180  
 aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
 cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccaaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420  
 ggaaagaaga gaccagtaga gcagtcacc ccaagaaccag actcctcctc gggcatcggc 480  
 aagaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540  
 tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600  
 aatacaatgg ctgcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660  
 gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780  
 tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccctc 840

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tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900
ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960
cagggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020
accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080
cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140
acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200
ccttcgcaga tgctgagaac cggaacaac ttccagttta cttacacctt cgaggacgtg 1260
cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320
gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgagc 1380
actctgggct tcagccaagg tgggcctaata acaatggcca atcaggcaaa gaactggctg 1440
ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500
aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaata 1560
cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttccc agtaacggga 1620
tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgcatgctc 1680
accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740
gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800
gccttaccgg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860
aagattcctc acacggacgg caacttcac ccgtctccgc tgatgggagg ctttggcctg 1920
aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980
accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040
gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100
tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160
tactctgaac cccgcccacat tggcacccgt tacctcacc gtaatctgta a 2211

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<210> 44
<211> 2211
<212> DNA
<213> new AAV serotype, clone hu.3

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<400> 44
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctac ctcaagtaca accacgccga cgagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgcgg cctggtttga ggaacactgt taagacggct 420
ccgggaaaaa agaggccggg agagcactct cctgtggagc cagactcctc ctcgggaacc 480
ggaaaagcgg gccagcagcc tgcaagaaaa agattaaatt ttggtcagac tggagacgca 540
gactccgtac ctgaccccca gcctctcggg cagccaccag cagccccctc tggctctggga 600
tctactacaa tggctacagg cagtggcgca ccaatggcag acaataacga gggtgccgat 660
ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctgga cgacagagtc 720
atcgccacca gcaccgaaac ctggggccctg cccacataca acaaccacct ctacaagcaa 780
atctccagcc aatcaggagc ctgcaacgac aaccactact ttggctacag cccccctgg 840
gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900
atcaacagca actggggatt ccggcccaaa agactcaact tcaagctctt taatattcaa 960
gtcaaagagg tcacgcagaa tgacggtagc acgacgattg ccaataacct taccagcacg 1020
gttcagggtg ttactgactc ggagtaccag ctcccgtacg tcccgggctc ggcgcacaa 1080
ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc cacagtatgg atacctcacc 1140

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ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt actgcctgga gtactttcct 1200  
 tctcagatgc tgcgtactgg aaacaacttt cagttcagct acacttttga agacgtgcct 1260  
 ttccacagca gctacgctca ctgccagagt ctggatcggc tgatgaatcc tctgatcgac 1320  
 cagtacctgt attatctgaa caagacacaa acaaatagtg gaactcttca gcagtctcgg 1380  
 ctactgttta gccaaagctgg accaaccaac atgtctcttc aagctaaaaa ctggctgcct 1440  
 ggaccttgct acagacagca gcgtctgtca aaacaggcaa acgacaataa caactgcaac 1500  
 tttccctgga ctgcagctac aaagtatcat ctaaattggcc gggactcgtt ggttaatcca 1560  
 ggaccagcta tggccagtca caaggatgac gaagaaaagt ttttcccat gcatggaacc 1620  
 ctgatatttg gtaaacaagg aacaaatgcc aacgacgcgg atttggaataa tgcacatgatt 1680  
 acagatgaag aagaaatcag gccccaat cccgtggcta cggagcagta cgggactgtg 1740  
 tcaataaatt tgcaaaactc aaacactggc ccaactacag gaactgtcaa tcaccaagga 1800  
 gcgttacctg gtatggtgtg gcaggatcga gacgtgtacc tgcagggacc catttgggcc 1860  
 aagattcctc acaccgatgg acactttcat ccttctccac tgatgggagg ttttggactc 1920  
 aaacaccgcg ctctcagat catgatcaaa agcactcccg ttccagccaa tcctcccaca 1980  
 aacttcagtt ctgccaagtt tgcttcttcc atcacacagt attccacggg acaggtcagc 2040  
 gtggagatcg agtgggagct gcagaaggag aacagcaaac gctggaatcc cgaaattcag 2100  
 tacacttcca actacaacaa gtctgttaat gtggacttta ctgtggacac taatggtgtg 2160  
 tattcagagc ctgcacctat tggcaccaga tacctgactc gtaattctgta a 2211

<210> 45  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.5

<400> 45  
 atggctgccg atggttatct tccagattgg ctgcaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc cggctcaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240  
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300  
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctctc gggaaccgga 480  
 aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540  
 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600  
 actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaadc 780  
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
 tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900  
 aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960  
 aaagagggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020  
 cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080  
 tgccctccgc cgtttccagc ggacgtcttc atggtccac agtatggata cctcacctg 1140  
 aacaacggga gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200  
 cagatgtctg gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260  
 cacagcagct acgtcacag ccagagctct gatcggctga tgaatcctct gatcgaccag 1320  
 tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380  
 ctgttttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

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ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcgcaa ggatgacgaa gaaaagtfff tccccatgca tggaaacctg 1620
atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740
aataatttgc aaaactcaaa cactgggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgatggaca ctttcatcct tctccactga tgggagggtt tggactcaaa 1920
caccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980
ttcagttctg ccaagtttgc ttttttcatc acacagtatt ccacgggaca ggtcagcggtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 46
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.1

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<400> 46
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaac tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc cgggtcaacg ggcagacgcc gcggccctcg agcacgaca ggcttacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggatct 600
actacaatgg ctacaggcag tggcgacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcca cagagtcata 720
accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaata 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcata 900
aacaacaact ggggattccg gcccaaaaaga ctcaacttca agctctttaa tattcaagtc 960
aaagagggtc cgcagaatgg cggtagcagc acgattgcca ataacctac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080
tgccctccgc cgtttccagc ggacgtcttc atgggtccac agtatggata cctcacctg 1140
aacaacggga gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttct 1200
cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260
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tacctgtatt atctgaacaa gacacaaaac aatagtggaa ctcttcagca gtctcggcta 1380
ctgttttagc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440
ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg gcaacaacaa cagcaacttt 1500
ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggg taatccagga 1560
ccagctatgg ccagtcacaa ggatgacgaa gaaaagtfff tccccatgca tggaaacctg 1620
atatttggtg aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680
gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

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aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800
ttacctggta tgggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaaag 1860
attcctcaca ccgatggaca ctttcaccc tctccactga cgggaggttt tggactcaaa 1920
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ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 47
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.4

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<400> 47
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgtc tcttgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctc gggaaccgga 480
aaagcggggc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggatct 600
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gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
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gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100  
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 48  
 <211> 2209  
 <212> DNA  
 <213> new AAV serotype, clone hu.2

<400> 48  
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 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
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<210> 49  
 <211> 2208

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu.25

&lt;400&gt; 49

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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac      180
aagggagagc cggcacaaga ggcagacgcc gcggccctcg agcacgaca ggcttacgac      240
cggcagctca acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt      300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag      360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg      420
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tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa      2208

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&lt;210&gt; 50

&lt;211&gt; 2208

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu.15

&lt;400&gt; 50

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atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga      60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactctac      180

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gccaaaaaga gggttcttga acctctgggc ttggttgggg agcctgttaa aacggctccg 420
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tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 51
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.16

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<400> 51
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aaggagagc cggctaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccg cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaccgga 480

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 actacaatgg ctacaggcag tggcgaccca gtggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
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<210> 52  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.18

<400> 52  
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 gacagcaggg gtcttgtgct tcctgggtac aagtacctg gacccttcaa cggactcgac 180  
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 tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggatct 600  
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 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.8

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<210> 54  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone rh.56

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<210> 55  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.7

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 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.10

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 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.11

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<210> 58

&lt;211&gt; 2208

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu.9

&lt;400&gt; 58

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gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat    2100
acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat    2160
tcagagcctt gccccattgg caccagatac ctgactcgta atctgtaa                    2208

```

&lt;210&gt; 59

&lt;211&gt; 2208

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu.12

&lt;400&gt; 59

```

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga    60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac    120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac    180

```



```

aaaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag ccccccacaag tttgggatct 600
actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660
gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaattc 780
tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt cactgtcac ttctcccac gtgattggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
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tgctcccg cgtttccagc ggacgtcttc atggtccac agtatggata cctcacctg 1140
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cagatgctgc gtactggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320
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ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tgggaccctg 1620
atatttggtg aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680
gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740
aataatttgc aaaactcaaa tactgggtcca actacagaaa atgtcaatca ccagggagcg 1800
ttacctggta tgggtgtggc ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860
attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920
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ttcagtctg ccaagtgtgc tttttcatc acacagtatt ccacgggcca ggtcagcgtg 2040
gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

```

```

<210> 60
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.23

```

```

<400> 60
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aaggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

```

```

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatac gatgg cttcaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaatac 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020
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tgccctccgc cgttccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
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cagatgcttc gtaccggaac caactttacc ttacgttaca cctttgaaga cgttcccttc 1260
catagcagct acgtccacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaact ccaagcggaa ccaccacgat gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctgaaactg gcttcctgga 1440
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gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
cttccaggca tggctctggc ggacagagac gtgtacctgc gggggcccat ctgggcaaag 1860
attccacaca cgagcggaca ttttcacccc tctccctca tgggcggatt tggacttaaa 1920
caccctctc cacaattct catcaagaac acccgggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtgtgc ttccttcac acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaatac tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

```

<210> 61  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.26

```

<400> 61
atggctgccc atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agtcaaacc tggcccacca ccaccaaac ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctc gcggagccag actcctcctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatac gatgg cttcaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatac 780

```

```

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggatttccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctccccg cgttcccagc agacgtcttc atgggtgccac agtatggata cctcaccctg 1140
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cagatgcttc gtaccggaaa caactttacc ttgagctaca cctttgaaga cgttccttct 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccagat gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctgaaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500
tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttctcagag cggggttctc 1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
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attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920
caccctctc cacaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtttgc ttcttctatc acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaatc tgttaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

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```

<210> 62
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.19

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```

<400> 62
atggctgccg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaac tggcccacca ccaccaagc ccgagagcg gcataaggac 120
gacagcaggg gtcttgctgc tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgtc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggagaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaagaga ttgaattttg gccagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctctg tctgggaact 600
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggtggggcga cagagtcattc 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggatttccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

```

```

tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttccttct 1200
cagatgcttc gtaccgga aaactttacc ttcagctaca ctttgaaga cgttcctttc 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380
cagttttctc aggcgggagc aagtgcatt cgggaccagt ctgaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgtattac 1500
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gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800
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gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccg aattcagtac 2100
acttccaact acaacaatc tgtaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 63
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.20

```

```

<400> 63
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gacagcaggg gtctgtgtct tcctgggtac aggtacctcg gacccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcttacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgtcga cgcggagttt 300
caggagcgtc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg 420
ggagaaaaga ggccggtaga gactctctc gcggagccag actcctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg accccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600
aatacagatg cttcaggcag tggcgacca atggcagaca ataacgagg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
cattttgact tcaacagatt cactgccac ttctccccc gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctacgttca agctctttaa cattcaagtc 960
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tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
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cagatgcttc gtaccgga aaactttacc ttcagctaca ctttgaaga cgttcctttc 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
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 tcgtggactg gagctaccaaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
 ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620  
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 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
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 caccctcttc cacaatttct catcaagaac accccgggtac ctgcgaatcc ttcgaccact 1980  
 ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacggggca ggtcagcggtg 2040  
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtag 2100  
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gcccatttgg cgccagatac ctgactcgta atctgtaa 2208

<210> 64  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.27

<400> 64  
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 cagtgggtgga agctcaaac tggcccacca ccacaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttctgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
 aaggagagcg cggctcaacga ggcagacgac gcggccctcg agcacgacaa ggcctacgac 240  
 cggcagctcg acagcggaga caaccggtac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480  
 aaagcgggac agcagcctgc aagaagaga ttgaattttg gtcagactgg agacgcagac 540  
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctctg tctgggaact 600  
 aatacagtag cttcaggcag tggcgacca atggcagaca ataacgaggc gcccgacgga 660  
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 tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
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 tgccttccgc cgttcccagc agactcttct atggtgccac agtatggata cctcaccctg 1140  
 aacaacggca gtcaggcggg aggacgctct tccttttact gcctggagta ctttcttctc 1200  
 cagatgcttc gtaccggaac caactttacc ttcagctaca cctttgaaga cgttcttctc 1260  
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 tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgat gtccaggctt 1380  
 cagttttctc aggccggagc aagtgcattt cgggaccagt ctgaaactg gcttcctgga 1440  
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgtattac 1500  
 tcgtggactg gagctaccaaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
 ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cgggggttctc 1620  
 gtcttttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca 1680

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gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct 1740
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attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920
caccctcttc cacaattctt catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980
ttcagtgcgg caaagtttgt ttccttcac acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100
acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 65
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.21

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<400> 65
atggctgccc atggttatct tccagattgg ctcgaggaca cctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggcccacca ccaccaagc cgcagagcg gcataaggac 120
gacagcaggg gtcttctgtct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aaggagagagc cggctcaacga ggcagacgcc gcggccctcg agcacgacaa ggcttacgac 240
cggcagctcg acagcggaga taaccctgac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcttc gggaaccgga 480
aaagcgggccc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccgccc tctcggacag ccaccagcag cccctcttg tctgggaact 600
aatacgatgg cttcaggcag tggcgacca atggcagaca ataacgaggg cggcgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaact 780
tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccaactgcca ttctccccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacgggt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttcccgc cgttcccagc agacgtcttc atgggtccac agtatggata cctcaccctg 1140
aacaacggca gtcaggcggg aggacgtctt tccttttact gcctggagta ctttcttct 1200
cagatgtctt gtaccggaaa caactttacc ttcagctaca ctttgaaga cgttcctttc 1260
catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag acaaaact ccaagcggaa ccaccagat gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctgaaactg gcttcttgga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgttac 1500
tcgtggactg gagctacca gtaccacctc aatggaagag actctctggt gaatccgggc 1560
ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttctcagag cggggttctc 1620
atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagg tatgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcggt 1800
cttccaggca tggctctggca ggacagagac gtgtacctgc aggggcccatt ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920
caccctcttc cacaattctt catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

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ttcagtgcgg	caaagtttgc	ttccttcac	acacagtact	ccacggggca	ggtcagcgtg	2040
gagatcgagt	gggagctgca	gaaggagaac	agcaaacgct	ggaatcccga	aattcagtac	2100
acttccaact	acaacaaatc	tgtaaatgtg	gactttactg	tggaactaa	tggtgtgtat	2160
tcagagcctc	gccccattgg	caccagatac	ctgactcgta	atctgtaa		2208

<210> 66  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.24

<400> 66		
atggctgccg	atggttatct	60
cagtgggtgga	agctcaaacc	120
gacagcaggg	gtcttgtgct	180
aagggagagc	cgggtcaacga	240
cggcagctcg	acagcggaga	300
caggagcgcc	ttaaagagga	360
gcaaaaaaga	ggattcttga	420
ggaaaaaaga	ggccggtaga	480
aaagcggggc	agcagcctgc	540
tcagtacctg	acccccggcc	600
aatacgatgg	cttcaggcag	660
gtgggtaatt	cctcgggaaa	720
accaccagca	cccgcacctg	780
tccagccagt	ctggagccag	840
tattttgact	tcaacagatt	900
aacaacaact	ggggattccg	960
aaagagggtca	cgcagaatga	1020
caggtgttta	ctgactcgga	1080
tgccctccgc	cgttcccagc	1140
aacaacggca	gtcaggcggt	1200
cagatgcttc	gtaccggaaa	1260
catagcagct	acgctcacag	1320
tacctgtatt	acttgagcag	1380
cagttttctc	aggccggagc	1440
ccctgttacc	gccagcagcg	1500
tcgtggactg	gagctacca	1560
ccagctatgg	ccagccacaa	1620
atctttggaa	aacaagactc	1680
gacgaagagg	aaatcaggac	1740
accaacctcc	agagcggcaa	1800
cttcagggca	tggctcggca	1860
attccacaca	cggacggaca	1920
caccctctc	cacaaattct	1980
ttcagtgcgg	caaagtttgc	2040
gagatcgagt	gggagctgca	2100
acttccaact	acaacaaatc	2160
tcagagcctc	gccccattgg	2208

<210> 67  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.22

<400> 67  
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttggtgt tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
 aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggccctacgac 240  
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480  
 aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540  
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600  
 aatacgtatg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagcga 660  
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggagg cagagtcac 720  
 accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaata 780  
 tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840  
 tattttgact tcaacagatt ccactgccac ttctcccccac gtgactggca aagactcatc 900  
 aacaacaact ggggattccg gccaagaga ctgagcttca agctctttaa cattcaagtc 960  
 aaagaggtca cgcagaatga cgttacgacg acgattgcca ataaccttac cagcacggtt 1020  
 cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
 tgccctccgc cgttcccgac agacgtcttc atggtgccac agtatggata cctcaccctg 1140  
 aacaacggca gtcaggcggg aggcagctct tccttttact gcctggagta ctttcttct 1200  
 cagacgcttc gtaccggaaa caactttacc ttacagtaca cctttgaaga cgttcttct 1260  
 catagcagct acgtcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320  
 tacctgtatt acttgagcag acaaaact ccaagcggaa ccaccagat gtccaggctt 1380  
 cagttttctc aggcgggagc aagtacatt cgggaccagt ctagaaactg gcttctctga 1440  
 ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgtattac 1500  
 tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560  
 ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttctcagag cgggggttctc 1620  
 atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaagggt tatgattaca 1680  
 gacgaagagg aatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800  
 cttccaggca tgggtctggca ggacagagac gtgtacctgc agggggcccat ctgggcaaa 1860  
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 caccctctc cacaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980  
 ttcagtgcgg caaagtgtgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040  
 gagatcgagt gggagctgca gaaggagaac agcaaagcgt ggaatcccga aattcagtac 2100  
 acttccaact acaacaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 68  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.28

<400> 68  
 atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
 cagtgggtgga aactcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120



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gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga gggttctgga acctctgagc ctgggtgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctccc gcagagccag attcctctc cggaaactgga 480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggaact 600
aatacgtagg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacgggt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccgag agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagt aggacgtctc tcattttact gcctagagta ctttcttct 1200
cagatgtctg gtaccggaaa caactttacc tttagctaca cttttgagga cgttcttct 1260
cacagcagct acgtcacag ccagagtttg gaccgtctca tgaatctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccagca gtccaggctt 1380
cagttttctc aggccggagc gaggacatt caggaccagt ctaggaaactg gcttcttga 1440
ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccggc 1560
ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttctcagag cggggttctt 1620
atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctaccgag atgtcaacac acaaggcgtt 1800
cttccaggca tggtcgggca agacagagac gtgtacctgc aggggcctac ttgggcaaa 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaa 1920
caccctctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgttc ttcttctatt acacagtact ccacggggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 69  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.29

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<400> 69
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaacc tggccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcaaaaaaga gggttctgga acctctgggc ctgggtgagg agcctgttaa gacggctccg 420

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ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggcca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccagc agacgtcttc atgggtgcc agtatggata cctcaccctg 1140
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cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaactg gcttctcgga 1440
ccctgttacc gtcagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cgggggttctt 1620
atctttggga agcaaggccc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800
cttcaggcca tggctcggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaa 1920
caccctctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgtgc ttccttcatt acacagtact ccacggggca ggtagcgtg 2040
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acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 70
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.30

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<400> 70
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgtgga agctcaaacc tggcccacca ccacaaagc ccgagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccctcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcgaggtt 300
caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gcaaaaaaga gggttctgga acctctgggc ctgggtgagg agcctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480
aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720

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accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780
tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020
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aacaacggga gtcaggcagt aggacgtctt tcattttact gcctagagta ctttccttct 1200
cagatgctgc gtaccggaaa cagctttacc ttcagctaca ctttgaggga cgttcctttc 1260
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tacctgtatt acttgagcag aacaaacct ccaagcggaa ccaccacgca gtccaggctt 1380
cagttttctc aggcgggagc gaggtagcatt cgggaccagt ctaggaaactg gcttcctgga 1440
ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg ccagccacaa agacgatgaa gaaaagttct ttcctcagag cggggttctt 1620
atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800
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attccacaca cggacggaca ttttcacccc tctccctca tgggcggatt tggacttaa 1920
caccctctc cagagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040
gagatcaggt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gcccatttgg caccagatac ctgactcgta atctgtaa 2208

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<210> 71
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.13

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<400> 71
atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60
cagtgggtgga agtcaaac ccggccacca ccaccaaac cgcagagcg gcataaggac 120
gacagcaggg gtcttggtct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480
aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacagatg cttcaggcag tggcgacca atggcagaca ataacgaggg cggcgacgga 660
gtgggttaatt cctcgggaaa ttggcattgc gattccacat ggtggggcga cagagtcac 720
accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaatc 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccgaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020

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 acttccaact acaacaaatc tgtaaatgtg gactttactg ttgacactaa tggcgtgtat 2160  
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<210> 72  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.34

<400> 72  
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 aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660  
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 tccagccaat caggagctc gaacgacaat cactactttg gctacagcac cccttggggg 840  
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acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160  
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 73  
<211> 2208  
<212> DNA  
<213> new AAV serotype, clone hu.35

<400> 73  
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240  
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300  
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gcgaaaaaga gggacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
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aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660  
gtgggttaatt cctcgggaaa ttggcattgc gattccacat ggatggcgca cagagtcac 720  
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780  
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aacaacaact ggggattccg acccaagaga ctcaacttca agtcttttaa cattcaagtc 960  
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ttcagtgcgg	caaagtgtgc	ttccttcctc	acacagtact	ccacgggaca	ggtcagcgtg	2040
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acttccaact	acaacaagtc	tgttaatgtg	gactttactg	tggacactaa	tggcgtgtat	2160
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 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.36

<400> 74						
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gacagcaggg	gtcttgtgct	tcctgggtac	aagtacctcg	gacccctcaa	cggactcgac	180
aagggagagc	cggtcaacga	ggcagacgcc	gcggccctcg	agcacgacaa	agcctacgac	240
cggcagctcg	acagcggaga	caacccgtac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggtactcga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
aaggcggggc	agcagcctgc	aagaaaaaga	ttgaattttg	gtcagactgg	agacgcagac	540
tcagtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	cgccgacgga	660
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aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttaa	cattcaagtc	960
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 gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100  
 acttccaact acaacaagtc cgttaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 75  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.33

<400> 75  
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 gacagcaggg gtcttggtct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
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 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagt 300  
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 gcgaaaaaga gggacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480  
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 accaccagca cccgaacctg ggcctgccc acctacaaca accacctcta caaacaatt 780  
 tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840  
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 acttccaact acaacaagtc tgtaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 76  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.45

<400> 76  
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 gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180  
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 acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 77  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.47

<400> 77  
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 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
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 ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctctctc gggaaccgga 480  
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 aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660  
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 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780  
 tccagccaat caggagcctc gaacgacagt cactactttg gctacagcac cccttggggg 840  
 tattttgact tcaacagatt ccaactgccac ttttaccac gtgactggca aagactcatc 900  
 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960  
 aaagaggta cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacggtt 1020  
 cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
 tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctcg 1140  
 aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttcttct 1200  
 cagatgtgc gtaccgaaa caactttacc tttagctaca cttttgagga cgttctttc 1260  
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 tttagtgagg caaagtttgc ttccttctc acacagtact ccacgggaca ggtcagcgtg 2040  
 gagatcaggt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100  
 acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 78  
 <211> 2211  
 <212> DNA  
 <213> new AAV serotype, clone hu.48

<400> 78  
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 gagtggtagg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120  
 gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480  
 aagacaggcc agcagcccgc taaaaagaga ctcaattttg gccagactgg cgactcagag 540  
 tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600  
 actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660  
 gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720  
 accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaacc 780  
 tccagtactt caacgggggc cagcaacgac aaccactact tcggctacgg caccctctgg 840  
 ggggtattttg atttcaacag attccactgc cacttttcac cactgtactg gcagcgactc 900  
 atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960  
 gtcgaggagg tcacgacgaa tgatggcgct acaaccatcg ctaataacct taccagcacg 1020  
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 ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320  
 caatacctgt attacctgaa cagaacacaa aatcagtcgg gaagtgccca aaacaaggac 1380  
 ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440  
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 gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800  
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 aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggagg ctttgactc 1920  
 aagaacccgc ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980  
 gagttttcag ctacaaagtt tgcttcattc atcaccat actccacagg acaagtgagt 2040  
 gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100  
 tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160  
 tatactgagc ctgcgcccat tggcaccctg taccttacc gtccctgta a 2211

<210> 79  
 <211> 2211  
 <212> DNA  
 <213> new AAV serotype, clone rh.71

<400> 79  
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 gagtgggtgg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120  
 gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cgactcagac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360  
 gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420  
 ggaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480  
 aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540  
 tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600  
 actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660  
 gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcca cagagtcac 720

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accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaadc 780
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gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900
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aagaaccgc ctctcagat cctcatcaa aacacgcctg ttcttgcaa tcctccggcg 1980
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tacacatcca attatgcaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccctg taccttacct gtcccctgta a 2211

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<210> 80
<211> 2214
<212> DNA
<213> new AAV serotype, clone hu.43

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<400> 80
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gagtgggtgg acctgaaacc tggagcccc aagcccaagg ccaaccagca gaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gaccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcttacgac 240
cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgcgagttt 300
caggagcgtc tgcaagaaga tacgcctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420
ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactctc cacgggcatc 480
ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540
gagtcagtcc ccgacctca accaatcgga gaaccaccag caggccccctc tggcttgga 600
tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660
ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720
atcacacca gcaccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780
atctccagtg cttaacggg ggccagcaac gacaaccact acttcggcta cagcaccctc 840
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caagtcaagg aggtcacgac gaatgatggc gtcacaacca tcgctaataa ccttaccagc 1020

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acggttcaag tcttctcggg ctcggagtag cagcttccgt acgtcctcgg ctctgcgcac 1080
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gcggagtttt cagctacaaa gtttgcttca ttcacaccc aatactccac aggacaagtg 2040
agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgtggaa tcccgaagtg 2100
cagtacacat ccaattatgc aaaatctgcc agcgttgatt ttactgtgga caacaatgga 2160
ctttatactg agcctcgcgc cattggcacc cgttacctta cccgtcccct gtaa 2214

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<210> 81
<211> 2211
<212> DNA
<213> new AAV serotype, clone hu.44

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<400> 81
atggctgctg atgggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcagacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacctttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaagaagc gggttctcga acctctcggg ctggttgagg aaggcgtgga gacggctcct 420
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aagacaggcc agcagcccgc taaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg atccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct 600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cccgacgga 660
gtgggtaatg cttcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
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tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccgt taccttacc gtcccctgta a 2211

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<210> 82
<211> 2211
<212> DNA
<213> new AAV serotype, clone hu.46

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<400> 82
atggctgccc acggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaac tggcccacca ccacaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgggc agtcttccag 360
gccaagaagc gggttctcga acctctcggc ctggttgagg aagcgctaa gacggctcct 420
ggaaagaaac gtccggtaga gcagtcgcca caagagccag actccccctc gggcatcggc 480
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 acagacgaag aggaatttaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740  
 gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800  
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<210> 83  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.17  
 <400> 83

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1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile

610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 84  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.6

<400> 84

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly



195	200	205
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 210 215 220		
Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val 225 230 235 240		
Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His 245 250 255		
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp 260 265 270		
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn 275 280 285		
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn 290 295 300		
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn 305 310 315 320		
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala 325 330 335		
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln 340 345 350		
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe 355 360 365		
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn 370 375 380		
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr 385 390 395 400		
Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr 405 410 415		
Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser 420 425 430		
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu 435 440 445		
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu 450 455 460		
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp 465 470 475 480		
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser 485 490 495		
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His 500 505 510		
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr 515 520 525		
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met 530 535 540		
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val 545 550 555 560		

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala  
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 85  
<211> 738  
<212> PRT  
<213> vp1, clone hu.42

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 86  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.38

<400> 86

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Arg Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 87  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.40  
 <400> 87

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Ser Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr

405 410 415  
 Thr Phe Glu Asp val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 88  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.37



&lt;400&gt; 88

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 89  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.39

<400> 89

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 90  
 <211> 738  
 <212> PRT  
 <213> vp1, clone AAV4407  
 <400> 90

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile

610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 91  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.41

<400> 91

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly

195	200	205
Gly Ala 210	Pro Met Ala Asp Asn 215	Asn Glu Gly Ala Asp 220
Ser Ser Gly Asn Trp 225	His Cys Asp Ser Thr 230	Trp Leu Gly Asp Arg Val 235
Ile Thr Thr Ser 245	Thr Arg Thr Trp Ala 250	Leu Pro Thr Tyr Asn Asn His 255
Leu Tyr Lys Gln 260	Ile Ser Asn Gly Thr 265	Ser Gly Gly Ser Thr Asn Asp 270
Asn Thr Tyr 275	Phe Gly Tyr Ser Thr 280	Pro Trp Gly Tyr Phe Asp Phe Asn 285
Arg Phe 290	His Cys His Phe Ser 295	Pro Arg Asp Trp Gln Arg Leu Ile Asn 300
Asn Asn Trp Gly Phe 305	Arg Pro Lys Arg Leu Ser 310	Phe Lys Leu Phe Asn 315
Ile Gln Val Lys 325	Glu Val Thr Gln Asn 330	Gly Thr Lys Thr Val Ala 335
Asn Asn Leu Thr 340	Ser Thr Ile Gln Val 345	Phe Thr Asp Ser Glu Tyr Gln 350
Leu Pro Tyr 355	Val Leu Gly Ser Ala 360	His Gln Gly Cys Leu Pro Pro Phe 365
Pro Ala 370	Asp Val Phe Met Ile 375	Pro Gln Tyr Gly Tyr Leu Thr Leu Asn 380
Asn Gly Ser Gln Ala 385	Val Gly Arg Ser Ser 390	Phe Tyr Cys Leu Glu Tyr 395
Phe Pro Ser Gln 405	Met Leu Arg Thr Gly 410	Asn Asn Phe Glu Phe Ser Tyr 415
Thr Phe Glu 420	Asp Val Pro Phe His 425	Ser Tyr Ala His Ser Gln Ser 430
Leu Asp 435	Arg Leu Met Asn Pro 440	Ile Asp Gln Tyr Leu Tyr Tyr Leu 445
Ser Arg Thr 450	Gln Ser Thr Gly 455	Gly Thr Gln Gly Thr Gln Gln Leu Leu 460
Phe Ser Gln Ala Gly 465	Pro Ala Asn Met Ser 470	Ala Gln Ala Lys Asn Trp 475
Leu Pro Gly Pro 485	Cys Tyr Arg Gln Gln 490	Arg Val Ser Thr Thr Leu Ser 495
Gln Asn Asn 500	Asn Ser Asn Phe Ala 505	Trp Thr Gly Ala Thr Lys Tyr His 510
Leu Asn Gly 515	Arg Asp Ser Leu Val 520	Asn Pro Gly Val Ala Met Ala Thr 525
His Lys 530	Asp Asp Glu Glu 535	Arg Phe Phe Pro Ser Ser Gly Val Leu Met 540
Phe Gly Lys Gln Gly 545	Ala Gly Arg Asp Asn 550	Val Asp Tyr Ser Ser Val 555



Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 92  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.40  
 <400> 92

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 93  
 <211> 731  
 <212> PRT  
 <213> vp1, clone pi.1

<400> 93

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln  
 145 150 155 160  
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser  
 165 170 175  
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
 180 185 190  
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
 195 200 205  
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His  
 210 215 220  
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
 225 230 235 240  
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
 465 470 475 480  
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe  
 485 490 495  
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
 500 505 510  
 Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
 515 520 525  
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
 530 535 540  
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
 545 550 555 560  
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
 565 570 575  
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
 580 585 590  
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
 595 600 605  
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
 610 615 620  
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
 625 630 635 640  
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
 645 650 655  
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
 660 665 670  
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
 675 680 685  
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
 690 695 700  
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
 705 710 715 720  
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 94  
 <211> 731  
 <212> PRT  
 <213> vp1, clone pi.3

<400> 94

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln  
 145 150 155 160  
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Pro Thr Gly Asp Ser Glu Ser  
 165 170 175  
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
 180 185 190  
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
 195 200 205  
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His  
 210 215 220  
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
 225 230 235 240  
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Thr Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn

420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460  
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
 465 470 475 480  
 Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Ser Asn Phe  
 485 490 495  
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
 500 505 510  
 Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
 515 520 525  
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
 530 535 540  
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
 545 550 555 560  
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
 565 570 575  
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
 580 585 590  
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
 595 600 605  
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
 610 615 620  
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
 625 630 635 640  
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
 645 650 655  
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
 660 665 670  
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
 675 680 685  
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
 690 695 700  
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
 705 710 715 720  
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 95  
 <211> 731  
 <212> PRT  
 <213> vp1, clone pi.2

<400> 95

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln  
 145 150 155 160  
 Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser  
 165 170 175  
 Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly  
 180 185 190  
 Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp  
 195 200 205  
 Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His  
 210 215 220  
 Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg  
 225 230 235 240  
 Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser  
 245 250 255  
 Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val  
 370 375 380



Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn  
 435 440 445  
 Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln  
 450 455 460  
 Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg  
 465 470 475 480  
 Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe  
 485 490 495  
 Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu  
 500 505 510  
 Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg  
 515 520 525  
 Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly  
 530 535 540  
 Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu  
 545 550 555 560  
 Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala  
 565 570 575  
 Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn  
 580 585 590  
 Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr  
 595 600 605  
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe  
 610 615 620  
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro  
 625 630 635 640  
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn  
 645 650 655  
 Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly  
 660 665 670  
 Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys  
 675 680 685  
 Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala  
 690 695 700  
 Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg  
 705 710 715 720  
 Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 96  
 <211> 738  
 <212> PRT

213> H<sub>2</sub>O, 100°C, 1h, 52

<400> 96

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140  
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160  
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175  
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190  
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205  
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220  
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240  
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255  
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270  
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285  
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300  
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
305 310 315 320  
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
325 330 335  
Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 97  
<211> 738  
<212> PRT  
<213> vp1, clone rh.53

<400> 97

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe

660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg  
 725 730 735  
 Asn Leu

<210> 98  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.70

<400> 98

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His

245                      250                      255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260                      265                      270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275                      280                      285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290                      295                      300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
305                      310                      315                      320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
325                      330                      335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
340                      345                      350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
355                      360                      365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
370                      375                      380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
385                      390                      395                      400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
405                      410                      415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
420                      425                      430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
435                      440                      445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
450                      455                      460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
465                      470                      475                      480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
485                      490                      495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
500                      505                      510

Leu Ser Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
515                      520                      525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
530                      535                      540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
545                      550                      555                      560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
565                      570                      575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
580                      585                      590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
595                      600                      605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 99  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.64  
 <400> 99

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190



Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu  
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr  
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 100  
<211> 738  
<212> PRT  
<213> vp1, clone rh.68  
<400> 100

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Pro Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Val Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 101  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.46

<400> 101

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 102  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.39

<400> 102

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Arg  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Ala Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Pro Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400

<210>	103
<211>	738
<212>	PRT



<213> "vp1, clone rh.49"

<400> 103

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Leu Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 104  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.51

<400> 104

Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Gln Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe

"660"

665

670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 105  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.57

&lt;400&gt; 105

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

245  
 250 255  
 Leu Tyr Lys Gln Thr Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 106  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.58

<400> 106

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560



Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 107  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.61

<400> 107

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 108  
 <211> 738  
 <212> PRT  
 <213> vp1, clone rh.50

<400> 108

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Gly Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 109  
 <211> 737  
 <212> PRT  
 <213> vpl, clone rh.45

<400> 109

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35

40

45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445  
 Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe  
 450 455 460  
 Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu  
 465 470 475 480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln  
 485 490 495  
 Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu  
 500 505 510  
 Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn  
 515 520 525  
 Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe  
 530 535 540  
 Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met  
 545 550 555 560  
 Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro  
 580 585 590  
 Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly  
 705 710 715 720  
 Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735  
 Leu

<210> 110  
 <211> 738  
 <212> PRT

&lt;213&gt; "vp1," clone rh.59"

&lt;400&gt; 110

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350



Pro Tyr Val<sub>355</sub> Leu Gly Ser Ala<sub>360</sub> His Gln Gly Cys Leu<sub>365</sub> Pro Pro Phe Pro  
 Ala Asp Val<sub>370</sub> Phe Met Ile Pro<sub>375</sub> Gln Tyr Gly Tyr Leu<sub>380</sub> Thr Leu Asn Asn  
 Gly Ser Gln Ser Val<sub>390</sub> Gly Arg Ser Ser Phe<sub>395</sub> Tyr Cys Leu Glu Tyr Phe<sub>400</sub>  
 Pro Ser Gln Met<sub>405</sub> Leu Arg Thr Gly Asn<sub>410</sub> Asn Phe Thr Phe Ser Tyr<sub>415</sub> Thr  
 Phe Glu Asp Val<sub>420</sub> Pro Phe His Ser<sub>425</sub> Ser Tyr Ala His Ser<sub>430</sub> Gln Ser Leu  
 Asp Arg Leu<sub>435</sub> Met Asn Pro Leu<sub>440</sub> Ile Asp Gln Tyr Leu<sub>445</sub> Tyr Tyr Leu Ala  
 Arg Thr Gln Ser Asn Ala<sub>455</sub> Gly Gly Thr Ala Gly<sub>460</sub> Asn Arg Glu Leu Gln  
 Phe Tyr Gln Gly Gly<sub>470</sub> Pro Thr Thr Met Ala<sub>475</sub> Glu Gln Ala Lys Asn Trp<sub>480</sub>  
 Leu Pro Gly Pro<sub>485</sub> Cys Tyr Arg Gln Gln<sub>490</sub> Arg Val Ser Thr Thr Leu Ser<sub>495</sub>  
 Gln Asn Asn<sub>500</sub> Ser Asn Phe Ala<sub>505</sub> Trp Thr Gly Ala Thr Lys Tyr His<sub>510</sub>  
 Leu Asn Gly<sub>515</sub> Arg Asp Ser Leu<sub>520</sub> Val Asn Pro Gly Val<sub>525</sub> Ala Met Ala Thr  
 Asn Lys<sub>530</sub> Asp Asp Glu Asp<sub>535</sub> Arg Phe Phe Pro Ser<sub>540</sub> Ser Gly Ile Leu Met  
 Phe Gly Lys Gln Gly<sub>550</sub> Ala Gly Lys Asp Asn<sub>555</sub> Val Asp Tyr Ser Asn Val<sub>560</sub>  
 Met Leu Thr Ser<sub>565</sub> Glu Glu Glu Ile Lys<sub>570</sub> Thr Thr Asn Pro Val<sub>575</sub> Ala Thr  
 Glu Gln Tyr Gly<sub>580</sub> Val Val Ala Asp<sub>585</sub> Asn Leu Gln Gln Gln<sub>590</sub> Asn Thr Ala  
 Pro Ile Val<sub>595</sub> Gly Ala Val Asn<sub>600</sub> Ser Gln Gly Ala Leu<sub>605</sub> Pro Gly Met Val  
 Trp Gln Asn Arg Asp Val<sub>615</sub> Tyr Leu Gln Gly Pro<sub>620</sub> Ile Trp Ala Lys Ile  
 Pro His Thr Asp Gly<sub>630</sub> Phe His Pro Ser<sub>635</sub> Leu Met Gly Gly Phe<sub>640</sub>  
 Gly Leu Lys His<sub>645</sub> Pro Pro Pro Gln Ile<sub>650</sub> Leu Ile Lys Asn Thr Pro Val<sub>655</sub>  
 Pro Ala Asp<sub>660</sub> Pro Thr Ala Phe<sub>665</sub> Asn Gln Ala Lys Leu<sub>670</sub> Asn Ser Phe  
 Ile Thr Gln Tyr Ser Thr Gly<sub>680</sub> Gln Val Ser Val Glu<sub>685</sub> Ile Glu Trp Glu  
 Leu Gln Lys Glu Asn Ser<sub>695</sub> Lys Arg Trp Asn Pro<sub>700</sub> Glu Ile Gln Tyr Thr  
 Ser Asn Tyr Tyr Lys<sub>710</sub> Ser Thr Asn Val Asp<sub>715</sub> Phe Ala Val Asn Thr Glu<sub>720</sub>

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 111  
<211> 737  
<212> PRT  
<213> vp1, clone rh.44  
<400> 111

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp  
65 70 75 80

Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
260 265 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile

660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735  
 Leu

<210> 112  
 <211> 737  
 <212> PRT  
 <213> vpl, clone rh.65

<400> 112

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Arg Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735  
 Leu

<210> 113  
 <211> 737  
 <212> PRT  
 <213> vp1, clone rh.67

<400> 113

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
565 570 575  
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
580 585 590  
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
595 600 605  
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
610 615 620  
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
625 630 635 640  
Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
645 650 655  
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
660 665 670  
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
675 680 685  
Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
690 695 700  
Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
705 710 715 720  
Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 114  
<211> 737  
<212> PRT  
<213> vp1, clone rh.62  
<400> 114

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15  
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30  
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45  
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60  
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80  
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95  
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110  
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125  
Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140



Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 115  
 <211> 737  
 <212> PRT  
 <213> vp1, clone rh.48

<400> 115

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln

450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 116  
 <211> 737  
 <212> PRT  
 <213> vp1, clone rh.54

<400> 116

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400

Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735  
 Leu

<210> 117  
 <211> 737  
 <212> PRT

&lt;213&gt; vpl, clone rh.55

&lt;400&gt; 117

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720



Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 118  
<211> 738  
<212> PRT  
<213> vp1, clone rh.47

<400> 118

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300

Asn 305 Asn Trp Gly Phe Arg 310 Pro Lys Arg Leu Ser 315 Phe Lys Leu Phe Asn 320  
 Ile Gln Val Lys Glu 325 Val Thr Gln Asn Glu 330 Gly Thr Lys Thr Ile 335 Ala  
 Asn Asn Leu Thr 340 Ser Thr Val Gln Val 345 Phe Ser Asp Ser Glu 350 Tyr Gln  
 Leu Pro Tyr 355 Val Leu Gly Ser Ala 360 His Gln Gly Cys Leu 365 Pro Pro Phe  
 Pro Ala 370 Asp Val Phe Met Ile 375 Pro Gln Tyr Gly Tyr 380 Leu Thr Leu Asn  
 Asn 385 Gly Ser Gln Ser Val 390 Gly Arg Ser Ser Phe 395 Tyr Cys Leu Glu Tyr 400  
 Phe Pro Ser Gln Met 405 Leu Arg Thr Gly Asn 410 Asn Phe Thr Phe Ser 415 Tyr  
 Thr Phe Glu Asp 420 Val Pro Phe His Ser 425 Ser Tyr Ala His Ser 430 Gln Ser  
 Leu Asp Arg 435 Leu Met Asn Pro Leu 440 Ile Asp Gln Tyr Leu 445 Tyr Tyr Leu  
 Ala Arg 450 Thr Gln Ser Asn Ala 455 Gly Gly Thr Ala Gly 460 Asn Arg Glu Leu  
 Gln 465 Phe Tyr Gln Gly Gly 470 Pro Thr Thr Met Ala 475 Glu Gln Ala Lys Asn 480  
 Trp Leu Pro Gly Pro 485 Cys Phe Arg Gln Gln 490 Arg Val Ser Lys Thr 495 Leu  
 Asp Gln Asn Asn 500 Asn Ser Asn Phe Ala 505 Trp Thr Gly Ala Thr 510 Lys Tyr  
 His Leu Asn 515 Gly Arg Asn Ser Leu 520 Val Asn Pro Gly Val 525 Ala Met Ala  
 Thr His 530 Lys Asp Asp Glu Glu 535 Arg Phe Phe Pro Ser 540 Ser Gly Val Leu  
 Ile 545 Phe Gly Lys Thr Gly 550 Ala Ala Asn Lys Thr 555 Thr Leu Glu Asn Val 560  
 Leu Met Thr Asn Glu 565 Glu Glu Ile Arg Pro 570 Thr Asn Pro Val Ala Thr 575  
 Glu Glu Tyr Gly 580 Thr Val Ser Ser Asn 585 Leu Gln Ala Ala Asn 590 Thr Ala  
 Ala Gln Thr 595 Gln Val Val Asn Asn 600 Gln Gly Ala Leu Pro 605 Gly Met Val  
 Trp Gln 610 Asn Arg Asp Val Tyr 615 Leu Gln Gly Pro Ile 620 Trp Ala Lys Ile  
 Pro 625 His Thr Asp Gly Asn 630 Phe His Pro Ser Pro 635 Leu Met Gly Gly Phe 640  
 Gly Leu Lys His Pro 645 Pro Pro Gln Ile Leu 650 Ile Lys Asn Thr Pro 655 Val  
 Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe

660

665

670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 119  
 <211> 737  
 <212> PRT  
 <213> vp1, clone rh.69

&lt;400&gt; 119

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His

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Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 120  
 <211> 735  
 <212> PRT  
 <213> vp1, clone rh.60

<400> 120

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560

Met Thr Asn Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
565 570 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
625 630 635 640

Leu Lys His Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Phe  
690 695 700

Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 121  
 <211> 736  
 <212> PRT  
 <213> vp1, clone hu.31

<400> 121

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
145 150 155 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
 260 265 270  
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp  
 370 375 380  
 Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu  
 405 410 415  
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445  
 Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
 450 455 460  
 Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
 465 470 475 480  
 Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
 485 490 495  
 Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
 500 505 510  
 Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys  
 515 520 525



Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
 530 535 540  
 Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
 545 550 555 560  
 Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
 565 570 575  
 Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
 580 585 590  
 Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
 625 630 635 640  
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val  
 705 710 715 720  
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 122  
 <211> 736  
 <212> PRT  
 <213> vp1, clone hu.32  
 <400> 122  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
 145 150 155 160  
 Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
 260 265 270  
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu  
 405 410 415  
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445  
 Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
 450 455 460  
 Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
 465 470 475 480  
 Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn

485 490 495  
 Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
 500 505 510  
 Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys  
 515 520 525  
 Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
 530 535 540  
 Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
 545 550 555 560  
 Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
 565 570 575  
 Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
 580 585 590  
 Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
 625 630 635 640  
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val  
 705 710 715 720  
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 123  
 <211> 736  
 <212> PRT  
 <213> capsid of hu.14\AAV9

<400> 123

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro  
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly  
 145 150 155 160  
 Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn  
 260 265 270  
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu  
 405 410 415  
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser  
 435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser  
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro  
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn  
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn  
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys  
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly  
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile  
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser  
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln  
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln  
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met  
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr  
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val  
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 124

<211> 735

<212> PRT

<213> vp1, clone hu.33

<400> 124

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 125  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.34  
 <400> 125  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser  
 370 375 380



Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

&lt;210&gt; 126

<211> 735  
 <212> PRT  
 <213> vp1, clone hu.36

<400> 126

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr

340										345										350										
Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	Leu	Pro	Pro	Phe	Pro	Ala	Asp															
		355					360					365																		
Val	Phe	Met	Val	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Asn	Gly	Ser															
	370					375					380																			
Gln	Ala	Ala	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro	Ser															
385					390					395					400															
Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Thr	Phe	Ser	Tyr	Thr	Phe	Glu															
			405						410					415																
Asp	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser	Leu	Gly	Arg															
		420						425					430																	
Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser	Arg	Thr															
		435				440						445																		
Asn	Thr	Pro	Ser	Gly	Thr	Thr	Thr	Gln	Ser	Arg	Leu	Gln	Phe	Ser	Gln															
	450					455					460																			
Ala	Gly	Ala	Ser	Asp	Ile	Arg	Asp	Gln	Ser	Arg	Asn	Trp	Leu	Pro	Gly															
465					470					475					480															
Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Lys	Thr	Ser	Ala	Asp	Asn	Asn															
				485					490					495																
Asn	Ser	Glu	Tyr	Ser	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His	Leu	Asn	Gly															
		500						505					510																	
Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Pro	Ala	Met	Ala	Ser	His	Lys	Asp															
		515					520					525																		
Asp	Glu	Glu	Lys	Phe	Phe	Pro	Gln	Ser	Gly	Val	Leu	Ile	Phe	Gly	Lys															
	530					535					540																			
Gln	Gly	Ser	Glu	Lys	Thr	Asn	Val	Asp	Ile	Glu	Lys	Val	Met	Ile	Thr															
545					550					555					560															
Asp	Glu	Glu	Glu	Ile	Arg	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Gln	Tyr															
			565						570					575																
Gly	Ser	Val	Ser	Thr	Asn	Leu	Gln	Arg	Gly	Asn	Arg	Gln	Ala	Ala	Thr															
		580						585					590																	
Ala	Asp	Val	Asn	Thr	Gln	Gly	Val	Leu	Pro	Gly	Met	Val	Trp	Gln	Asp															
		595					600					605																		
Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr															
	610				615						620																			
Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu	Lys															
625					630					635					640															
His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala	Asn															
			645						650					655																
Pro	Ser	Thr	Thr	Phe	Ser	Ala	Ala	Lys	Phe	Ala	Ser	Phe	Ile	Thr	Gln															
		660						665					670																	
Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln	Lys															
	675						680					685																		
Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn	Tyr															
	690					695					700																			

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 127  
<211> 735  
<212> PRT  
<213> vp1, clone hu.45

<400> 127

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 128  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.47  
 <400> 128  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr  
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 129  
 <211> 735  
 <212> PRT  
 <213> vpl, clone hu.13

<400> 129

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240



Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp

595                      600                      605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610                      615                      620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625                      630                      635                      640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645                      650                      655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725                      730                      735  
  
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 <212> PRT  
 <213> vp1, clone hu.28  
  
 <400> 130  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20                      25                      30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50                      55                      60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115                      120                      125  
 Leu Ser Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130                      135                      140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145                      150                      155                      160  
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165                      170                      175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180                      185                      190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly

195	200	205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser 210 215 220		
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile 225 230 235 240		
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 245 250 255		
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr 260 265 270		
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His 275 280 285		
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp 290 295 300		
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val 305 310 315 320		
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu 325 330 335		
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr 340 345 350		
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp 355 360 365		
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser 370 375 380		
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 385 390 395 400		
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu 405 410 415		
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg 420 425 430		
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr 435 440 445		
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln 450 455 460		
Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser Arg Asn Trp Leu Pro Gly 465 470 475 480		
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn 485 490 495		
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly 500 505 510		
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp 515 520 525		
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 530 535 540		
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 545 550 555 560		

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 131  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.30

<400> 131

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160

165 170 175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
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 <212> PRT  
 <213> vp1, clone hu.29  
 <400> 132  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
  
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 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.19  
  
 <400> 133  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95



Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln

450                      455                      460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465                      470                      475                      480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
                     485                      490                      495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
                     500                      505                      510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
                     515                      520                      525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
                     530                      535                      540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545                      550                      555                      560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
                     565                      570                      575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
                     580                      585                      590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
                     595                      600                      605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
                     610                      615                      620  
 Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys  
 625                      630                      635                      640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
                     645                      650                      655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
                     660                      665                      670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
                     675                      680                      685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
                     690                      695                      700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705                      710                      715                      720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
                     725                      730                      735

<210> 134  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.20

<400> 134

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
                     20                      25                      30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
                     35                      40                      45  
 Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Ala Ala Pro Gly Glu Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
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 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
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 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
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 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
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 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
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 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
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 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
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 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
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 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
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 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
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 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
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 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
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 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
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 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr



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305	310	315	320
Lys Glu Val Thr	Gln Asn Asp Gly Thr	Thr Thr Ile Ala Asn Asn Leu	
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His Pro Pro Pro	Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn		
	645	650	655
Pro Ser Thr	Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln		
	660	665	670

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Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
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 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
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Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
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 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
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 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
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 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
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 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
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 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 142  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.5  
 <400> 142  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly 130 Leu Val Glu Glu Pro 135 Val Lys Thr Ala Pro 140 Gly Lys Lys Arg  
 Pro 145 Val Glu His Ser 150 Pro Val Glu Pro Asp 155 Ser Ser Gly Thr Gly 160  
 Lys Ala Gly Gln Gln 165 Pro Ala Arg Lys 170 Arg Leu Asn Phe Gly Gln Thr 175  
 Gly Asp Ala 180 Asp Ser Val Pro Asp 185 Pro Gln Pro Leu Gly Gln Pro Pro 190  
 Ala Ala Pro 195 Ser Gly Leu Gly Ser 200 Thr Thr Met Ala 205 Thr Gly Ser Gly  
 Ala Pro 210 Met Ala Asp Asn 215 Asn Glu Gly Ala Asp 220 Gly Val Gly Asn Ser  
 Ser 225 Gly Asn Trp His 230 Cys Asp Ser Gln Trp 235 Leu Gly Asp Arg Val Ile 240  
 Thr Thr Ser Thr 245 Arg Thr Trp Ala Leu 250 Pro Thr Tyr Asn Asn His 255 Leu  
 Tyr Lys Gln 260 Ile Ser Ser Gln Ser 265 Gly Ala Ser Asn Asp 270 Asn His Tyr  
 Phe Gly 275 Tyr Ser Thr Pro Trp 280 Gly Tyr Phe Asp Phe 285 Asn Arg Phe His  
 Cys 290 His Phe Ser Pro Arg 295 Asp Trp Gln Arg Leu 300 Ile Asn Asn Asn Trp  
 Gly 305 Phe Arg Pro Lys 310 Arg Leu Asn Phe Lys 315 Leu Phe Asn Ile Gln Val 320  
 Lys Glu Val Thr 325 Gln Asn Asp Gly Thr 330 Thr Thr Ile Ala Asn 335 Asn Leu  
 Thr Ser Thr 340 Val Gln Val Phe Thr 345 Asp Ser Glu Tyr Gln 350 Leu Pro Tyr  
 Val Leu 355 Gly Ser Ala His Gln 360 Gly Cys Leu Pro Pro 365 Phe Pro Ala Asp  
 Val 370 Phe Met Val Pro Gln 375 Tyr Gly Tyr Leu Thr 380 Leu Asn Asn Gly Ser  
 Gln 385 Ala Val Gly Arg Ser 390 Ser Phe Tyr Cys 395 Leu Glu Tyr Phe Pro Ser 400  
 Gln Met Leu Arg 405 Thr Gly Asn Asn Phe 410 Gln Phe Ser Tyr Thr 415 Phe Glu  
 Asp Val Pro 420 Phe His Ser Ser Tyr 425 Ala His Ser Gln Ser 430 Leu Asp Arg  
 Leu Met 435 Asn Pro Leu Ile Asp 440 Gln Tyr Leu Tyr Tyr 445 Leu Asn Lys Thr  
 Gln 450 Thr Asn Ser Gly Thr 455 Leu Gln Gln Ser Arg 460 Leu Leu Phe Ser Gln  
 Ala 465 Gly Pro Thr Asn Met 470 Ser Leu Gln Ala 475 Lys Asn Trp Leu Pro Gly 480  
 Pro Cys Tyr Arg 485 Gln Gln Arg Leu Ser 490 Lys Gln Ala Asn Asp 495 Asn Asn

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 143  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.2

<400> 143

Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn Arg Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 144  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.1

<400> 144

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg



420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 145  
 <211> 736  
 <212> PRT  
 <213> vp1, clone hu.3

<400> 145

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro

-20-

25

30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys  
 130 135 140  
 Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr  
 145 150 155 160  
 Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val  
 225 230 235 240  
 Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Cys Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys  
 435 440 445  
 Thr Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser  
 450 455 460  
 Gln Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn  
 485 490 495  
 Asn Asn Cys Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn  
 500 505 510  
 Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly  
 530 535 540  
 Lys Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Gln  
 565 570 575  
 Tyr Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr  
 580 585 590  
 Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys His Pro Pro Pro Gln Ile Met Ile Lys Ser Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Ser Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val  
 705 710 715 720  
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 146  
 <211> 735  
 <212> PRT

2133 vpl; clone hu.25

<400> 146

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asn Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Pro Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Asn Asn Gly Val Tyr  
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 147  
<211> 735  
<212> PRT  
<213> vp1, clone hu.15

<400> 147

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro  
50 55 60

Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Leu Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys

675

680

685

Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 148  
<211> 735  
<212> PRT  
<213> vp1, clone hu.16  
<400> 148

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His



275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asp Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 149  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.18

<400> 149

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Ser Gly Ser Gly  
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Leu Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu  
 725 730 735

<210> 150  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.7

<400> 150

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
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 <212> PRT  
 <213> vp1, clone hu.8  
 <400> 151  
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 Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys

530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
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 <213> vp1, clone rh.56  
  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg



130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
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 <212> PRT  
 <213> vp1, clone hu.11  
 <400> 153  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp<sup>100</sup> Ala<sup>101</sup> Glu<sup>102</sup> Phe<sup>103</sup> Gln<sup>104</sup> Glu<sup>105</sup> Arg<sup>106</sup> Leu<sup>107</sup> Lys<sup>108</sup> Glu<sup>109</sup> Asp<sup>110</sup> Thr<sup>111</sup> Ser<sup>112</sup> Phe<sup>113</sup> Gly<sup>114</sup> Gly<sup>115</sup>  
 Asn<sup>116</sup> Leu<sup>117</sup> Gly<sup>118</sup> Arg<sup>119</sup> Ala<sup>120</sup> Val<sup>121</sup> Phe<sup>122</sup> Gln<sup>123</sup> Ala<sup>124</sup> Lys<sup>125</sup> Lys<sup>126</sup> Arg<sup>127</sup> Val<sup>128</sup> Leu<sup>129</sup> Glu<sup>130</sup> Pro<sup>131</sup>  
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 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly  
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 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
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 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
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 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
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 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
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 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
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 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
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 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
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 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
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 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
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 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
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 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
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 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
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 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
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 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
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 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
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 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
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 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
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 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
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 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
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 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
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 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr  
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 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
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 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
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 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser

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Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
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Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
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Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
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Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
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Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
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Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
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Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
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Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
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Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
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Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
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His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
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Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
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Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
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Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
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 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
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 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
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 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
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 Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
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Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
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Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
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Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
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Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr  
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Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
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Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
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His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
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Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
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Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys  
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Gly Arg Glu 515 Ser Ile Ile Asn Pro 520 Gly Thr Ala Met Ala 525 Ser His Lys

Asp 530 Glu Asp Lys Phe 535 Phe Pro Met Ser Gly Val 540 Met Ile Phe Gly

Lys 545 Glu Ser Ala Gly Ala 550 Ser Asn Thr Ala Leu 555 Asp Asn Val Met Ile

Thr Asp Glu Glu 565 Ile Lys Ala Thr Asn 570 Pro Val Ala Thr Glu 575 Arg

Phe Gly Thr Val 580 Ala Val Asn Phe Gln 585 Ser Ser Ser Thr Asp 590 Pro Ala

Thr Gly Asp 595 Val His Ala Met Gly 600 Ala Leu Pro Gly Met 605 Val Trp Gln

Asp 610 Arg Asp Val Tyr Leu Gln 615 Gly Pro Ile Trp Ala 620 Lys Ile Pro His

Thr Asp Gly His Phe 630 His Pro Ser Pro Leu Met 635 Gly Gly Phe Gly Leu 640

Lys Asn Pro Pro 645 Pro Gln Ile Leu Ile Lys 650 Asn Thr Pro Val Pro 655 Ala

Asn Pro Pro Ala 660 Glu Phe Ser Ala Thr 665 Lys Phe Ala Ser Phe 670 Ile Thr

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Lys 690 Glu Asn Ser Lys Arg Trp 695 Asn Pro Glu Val Gln 700 Tyr Thr Ser Asn

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&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; vp1, clone rh.43

&lt;400&gt; 163

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Asn Leu Gly	Arg Ala Val Phe	Gln <sub>120</sub> Ala Lys Lys Arg Val	Leu <sub>125</sub> Glu Pro
Leu Gly	Leu Val Glu Glu	Gly <sub>135</sub> Ala Lys Thr Ala	Pro <sub>140</sub> Gly Lys Lys Arg
Pro Val Glu Gln Ser	Pro <sub>150</sub> Gln Glu Pro Asp	Ser <sub>155</sub> Ser Ser Gly Ile	Gly <sub>160</sub>
Lys Lys Gly Gln	Gln <sub>165</sub> Pro Ala Arg Lys	Arg <sub>170</sub> Leu Asn Phe Gly	Gln <sub>175</sub> Thr
Gly Asp Ser	Glu Ser Val Pro Asp	Pro <sub>185</sub> Gln Pro Leu Gly	Glu <sub>190</sub> Pro Pro
Ala Ala Pro	Ser Gly Val Gly	Pro <sub>200</sub> Asn Thr Met Ala	Ala <sub>205</sub> Gly Gly Gly
Ala Pro Met Ala Asp Asn	Asn <sub>215</sub> Glu Gly Ala Asp	Gly <sub>220</sub> Val Gly Ser Ser	
Ser Gly Asn Trp His	Cys <sub>230</sub> Asp Ser Thr Trp	Leu <sub>235</sub> Gly Asp Arg Val	Ile <sub>240</sub>
Thr Thr Ser Thr	Arg <sub>245</sub> Thr Trp Ala Leu	Pro <sub>250</sub> Thr Tyr Asn Asn	His <sub>255</sub> Leu
Tyr Lys Gln	Ile <sub>260</sub> Ser Asn Gly Thr	Ser <sub>265</sub> Gly Gly Ala Thr	Asn <sub>270</sub> Asp Asn
Thr Tyr Phe	Gly Tyr Ser Thr	Pro <sub>280</sub> Trp Gly Tyr Phe	Asp <sub>285</sub> Phe Asn Arg
Phe His Cys His Phe Ser	Pro <sub>295</sub> Arg Asp Trp Gln	Arg <sub>300</sub> Leu Ile Asn Asn	
Asn Trp Gly Phe Arg	Pro <sub>310</sub> Lys Arg Leu Ser	Phe <sub>315</sub> Lys Leu Phe Asn	Ile <sub>320</sub>
Gln Val Lys Glu	Val <sub>325</sub> Thr Gln Asn Glu	Gly <sub>330</sub> Thr Lys Thr Ile	Ala <sub>335</sub> Asn
Asn Leu Thr	Ser <sub>340</sub> Thr Ile Gln Val	Phe <sub>345</sub> Thr Asp Ser Glu	Tyr <sub>350</sub> Gln Leu
Pro Tyr Val	Leu Gly Ser Ala	His <sub>360</sub> Gln Gly Cys Leu	Pro <sub>365</sub> Pro Phe Pro
Ala Asp Val	Phe Met Ile	Pro <sub>375</sub> Gln Tyr Gly Tyr	Leu <sub>380</sub> Thr Leu Asn Asn
Gly Ser Gln Ala Val	Gly <sub>390</sub> Arg Ser Ser Phe	Tyr <sub>395</sub> Cys Leu Glu Tyr	Phe <sub>400</sub>
Pro Ser Gln Met	Leu <sub>405</sub> Arg Thr Gly Asn	Asn <sub>410</sub> Phe Gln Phe Thr	Tyr <sub>415</sub> Thr
Phe Glu Asp	Val <sub>420</sub> Pro Phe His Ser	Ser <sub>425</sub> Tyr Ala His Ser	Gln <sub>430</sub> Ser Leu



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 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln  
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 Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp  
 530 535 540  
 Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu  
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 Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu  
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 Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln  
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 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
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 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
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 645 650 655  
 Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr  
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 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
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 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
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 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
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 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
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 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
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 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
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 <211> 3161  
 <212> DNA  
 <213> new AAV serotype, clone hu 136.1

<400> 165

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 <211> 3162  
 <212> DNA  
 <213> new AAV serotype, clone hu 140.1

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 <211> 3164  
 <212> DNA  
 <213> new AAV serotype, clone hu 140.2

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<211> 3159

<212> DNA

<213> new AAV serotype, clone hu 147.2

<400> 168

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 <211> 3156  
 <212> DNA  
 <213> new AAV serotype, clone hu 147.3

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 <211> 3158  
 <212> DNA  
 <213> new AAV serotype, clone hu 161.10

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 <211> 3167  
 <212> DNA  
 <213> new AAV serotype, clone hu 172.1

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 <211> 3161  
 <212> DNA  
 <213> new AAV serotype, clone hu 172.2

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 <212> DNA  
 <213> new AAV serotype, clone hu 173.4

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 <211> 3159  
 <212> DNA  
 <213> new AAV serotype, clone hu 161.8

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 <211> 3172  
 <212> DNA  
 <213> new AAV serotype, clone hu 173.8

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&lt;210&gt; 176

&lt;211&gt; 3160

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu 145.1

&lt;400&gt; 176

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&lt;211&gt; 3161

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu 156.1

&lt;400&gt; 179

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 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
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 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
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 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly  
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 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
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 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
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 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly  
 450 455 460  
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile  
 530 535 540  
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 184  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.60

<400> 184

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 185  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.61

<400> 185

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175



Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys

530

535

540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 186  
 <211> 734  
 <212> PRT  
 <213> vp1, clone hu.53

<400> 186

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala  
 450 455 460  
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn  
 485 490 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg  
 500 505 510  
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp  
 515 520 525  
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu  
 530 535 540  
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp  
 545 550 555 560  
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly  
 565 570 575  
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu  
 580 585 590  
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg  
 595 600 605  
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625 630 635 640  
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
 675 680 685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
 690 695 700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705 710 715 720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730  
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 <211> 734  
 <212> PRT  
 <213> vpl, clone hu.55  
 <400> 187  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Gly Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala  
 450 455 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg  
 500 505 510  
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp  
 515 520 525  
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu  
 530 535 540  
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp  
 545 550 555 560  
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly  
 565 570 575  
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu  
 580 585 590  
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg  
 595 600 605  
 Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625 630 635 640  
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
 675 680 685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
 690 695 700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705 710 715 720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730  
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 <211> 734  
 <212> PRT  
 <213> vp1, clone hu.54  
 <400> 188  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Gly Leu Asp Arg  
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435 440 445  
 Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala  
 450 455 460  
 Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro  
 465 470 475 480  
 Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn  
 485 490 495  
 Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Gly  
 500 505 510  
 Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp  
 515 520 525  
 Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu  
 530 535 540  
 Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp  
 545 550 555 560  
 Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly  
 565 570 575  
 Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu  
 580 585 590  
 Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg  
 595 600 605  
 Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625 630 635 640  
 Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
 675 680 685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
 690 695 700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705 710 715 720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 189  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.49

<400> 189

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30



Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser

"385' 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
595 600 605

Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 190  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.51

&lt;400&gt; 190

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 191  
<211> 735  
<212> PRT  
<213> vp1, clone hu.52

<400> 191

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Arg His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Ser Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 192  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.56  
 <400> 192  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn



645

650

655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 193  
 <211> 734  
 <212> PRT  
 <213> vp1, clone hu.57  
 <400> 193

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys  
 20 25 30  
 Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly  
 35 40 45  
 Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val  
 50 55 60  
 Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg  
 65 70 75 80  
 Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
 85 90 95  
 Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn  
 100 105 110  
 Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu  
 115 120 125  
 Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro  
 130 135 140  
 Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly Lys  
 145 150 155 160  
 Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly  
 165 170 175  
 Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala  
 180 185 190  
 Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala  
 195 200 205  
 Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser  
 210 215 220  
 Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr  
 225 230 235 240  
 Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr

245  
 Lys Gln Ile Ser<sub>260</sub> Ser Gln Ser Gly Ala<sub>265</sub> Ser Asn Asp Asn His<sub>270</sub> Tyr Phe  
 Gly Tyr Ser<sub>275</sub> Thr Pro Trp Gly Tyr<sub>280</sub> Phe Asp Phe Asn Arg<sub>285</sub> Phe His Cys  
 His Phe<sub>290</sub> Ser Pro Arg Asp Trp<sub>295</sub> Gln Arg Leu Ile Asn<sub>300</sub> Asn Asn Trp Gly  
 Phe Arg Pro Lys Arg Leu<sub>310</sub> Asn Leu Lys Leu Phe<sub>315</sub> Asn Ile Gln Val Lys<sub>320</sub>  
 Glu Val Thr Gln Asn<sub>325</sub> Asp Gly Thr Thr Thr<sub>330</sub> Ile Ala Asn Asn Leu<sub>335</sub> Thr  
 Ser Thr Val Gln<sub>340</sub> Val Phe Thr Asp Leu<sub>345</sub> Glu Tyr Gln Leu Pro<sub>350</sub> Tyr Val  
 Leu Gly Ser<sub>355</sub> Ala His Gln Gly Cys<sub>360</sub> Leu Pro Pro Phe Pro<sub>365</sub> Ala Asp Val  
 Phe Met<sub>370</sub> Val Pro Gln Tyr Gly<sub>375</sub> Tyr Leu Thr Leu Asn<sub>380</sub> Asn Gly Ser Gln  
 Ala Val Gly Arg Ser<sub>390</sub> Phe Tyr Cys Leu Glu<sub>395</sub> Tyr Phe Pro Ser Gln<sub>400</sub>  
 Met Leu Arg Thr Gly<sub>405</sub> Asn Asn Phe Thr Phe<sub>410</sub> Ser Tyr Thr Phe Glu<sub>415</sub> Asp  
 Val Pro Phe His<sub>420</sub> Ser Ser Tyr Ala His<sub>425</sub> Ser Gln Ser Leu Asp<sub>430</sub> Arg Leu  
 Met Asn Pro<sub>435</sub> Leu Ile Asp Gln Tyr<sub>440</sub> Leu Tyr Tyr Leu Ser<sub>445</sub> Arg Thr Asn  
 Thr Pro Ser Gly Thr Thr Thr<sub>455</sub> Gln Ser Arg Leu Gln<sub>460</sub> Phe Ser Gln Ala  
 Gly Ala Ser Asp Ile Arg<sub>470</sub> Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro<sub>480</sub>  
 Cys Tyr Arg Gln Gln<sub>485</sub> Arg Val Ser Lys Thr<sub>490</sub> Ala Ala Asp Asn Asn<sub>495</sub> Asn  
 Gly Glu Tyr Ser<sub>500</sub> Trp Thr Gly Ala Thr<sub>505</sub> Lys Tyr His Leu Asn<sub>510</sub> Gly Arg  
 Asp Ser Leu<sub>515</sub> Val Asn Pro Gly Pro<sub>520</sub> Ala Met Ala Ser His<sub>525</sub> Lys Asp Asp  
 Glu Glu<sub>530</sub> Lys Phe Phe Pro Gln<sub>535</sub> Ser Gly Val Leu Ile<sub>540</sub> Phe Gly Lys Gln  
 Gly Ser Glu Lys Thr Asn<sub>550</sub> Val Asp Ile Glu Lys<sub>555</sub> Val Met Ile Thr Asp<sub>560</sub>  
 Glu Glu Glu Ile Arg<sub>565</sub> Thr Thr Asn Pro Val<sub>570</sub> Ala Thr Glu Gln Tyr<sub>575</sub> Gly  
 Ser Val Ser Thr<sub>580</sub> Asn Leu Gln Ser Gly<sub>585</sub> Asn Thr Arg Ala Ala<sub>590</sub> Thr Ser  
 Asp Val Asn<sub>595</sub> Thr Gln Gly Val Leu<sub>600</sub> Pro Gly Met Val Trp<sub>605</sub> Gln Asp Arg

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His  
 625 630 640  
 Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu  
 675 680 685  
 Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn  
 690 695 700  
 Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser  
 705 710 715 720  
 Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730

<210> 194  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.58

<400> 194

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asp His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 195  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.63  
 <400> 195  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Pro Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 196  
 <211> 735  
 <212> PRT  
 <213> vp1, clone hu.64

<400> 196

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
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 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155  
 Lys Ala Gly Gln Gln Pro Ala Arg Arg Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly



500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
  
 <210> 197  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.66  
  
 <400> 197  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser  
 420 425 430  
 Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 198  
 <211> 738  
 <212> PRT  
 <213> vp1, clone hu.67

<400> 198

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu  
 35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415

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Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly  
 580 585 590  
 Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 199  
 <211> 2175  
 <212> DNA  
 <213> adeno-associated virus serotype 5

<400> 199

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 gccctgtggtc ttgtgctgcc tgggtataac tatctcggac ccggaacagg tctcgatcga 180  
 ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240  
 cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300  
 gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360  
 aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggccctacc 420  
 ggaaagcggg tagacgacca ctttccaaaa agaaagaagg ctccggaccga agaggactcc 480  
 aagccttcca cctcgtcaga cgccgaagct ggaccagcg gatcccagca gctgcaaatc 540  
 ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600  
 ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660  
 gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgcc 720  
 agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780  
 aacgcctact ttggatacag caccctctgg gggtaacttg actttaaccg cttccacagc 840  
 cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg 900  
 tccctcagag tcaaatctt caacattcaa gtcaaaggagg tcacgggtgca ggactccacc 960  
 accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020  
 ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080  
 ttacgctgc cgagtagcgg ttacgagcg ctgaaccgag acaacacaga aaatcccacc 1140  
 gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200  
 aactttgagt ttacctacaa ctttgaggag gtgccccttc actccagctt cgctccaggt 1260  
 cagaacctgt tcaagctggc caaccgctg gtggaccagt acttgtagc cttcgtgagc 1320  
 acaataaca ctggcggagt ccagttcaac aagaacctg ccgggagata cgccaacacc 1380  
 taaaaaact ggttcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg 1440  
 gtcaaccgag ccagtgtcag cgccttcgac acgaccaata ggatggagct cgaggcgagc 1500  
 agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560  
 tatgccctgg agaactat gatcttcaac agccagccgg cgaaccggg caccaccgcc 1620  
 acgtacctcg agggcaacat gctcatcacc agcagagagc agacgcagcc ggtgaaccgc 1680  
 gtggcgtaga acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc 1740  
 gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800  
 gtgtacctc aaggacctat ctgggccaa atccagaga cgggggagca ctttcacccc 1860  
 tctccggcca tgggcggatt cggactcaa caccaccgc ccatgatgct catcaagaac 1920  
 acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980  
 cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040  
 aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100  
 tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160  
 acccgacccc ttttaa 2175

<210> 200  
 <211> 2211  
 <212> DNA  
 <213> adeno-associated virus, serotype 3-3

<400> 200  
 atggctgctg acggttatct tccagattgg ctgaggaca acctttctga aggcattcgt 60  
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 aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gaccgggtaa cggactcgac 180  
 aaaggagagc cggtaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240  
 cagcagctca aggcgggtga caaccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360  
 gccaaaaaga ggatccttga gcctcttggg ctggttgagg aagcagctaa aacggctcct 420  
 ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tgggtgtggc 480  
 aaatcgggca aacagcctgc cagaaaaaga cttaaatttcg gtcagactgg agactcagag 540  
 tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600  
 aatacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaggg tgccgatgga 660  
 gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcac 720  
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 gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500  
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 actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040  
 gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100  
 tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160  
 tatagtgaac ctgcacctat tggaaccggg tatctcacac gaaacttgta a 2211

<210> 201  
 <211> 2205  
 <212> DNA  
 <213> adeno-associated virus, serotype 4-4

<400> 201  
 atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60  
 tgggtggcgc tgcaacctgg agccccctaaa cccaaggcaa atcaacaaca tcaggacaac 120  
 gctcggggtc ttgtgcttcc ggggttcaaaa tacctcggac ccggcaacgg actcgacaag 180  
 ggggaacctg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240  
 cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300  
 cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360  
 aaaaagaggg ttcttgaacc tcttggctcg gttgagcaag cgggtgagac ggctcctgga 420  
 aagaagagac cgttgattga atccccccag cagcccact cctccacggg tatcggcaaa 480  
 aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540  
 ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgaat gcgtgcagca 600

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" gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660
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tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780
aacacctaca acggattctc cccccctgg ggatactttg acttcaaccg cttccactgc 840
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gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960
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gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740
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cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860
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ccgcctctct aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980
agctctactc cggtaaactc cttcattact cagtacagca ctggccagggt gtcggtgcag 2040
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tccaactacg gacagcaaaa ctctctgttg tgggtctccg atgaggctgg gaaatacact 2160
gagcctaggg ctatcggtag ccgtacctc acccaccacc tgtaa 2205

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<210> 202
<211> 2211
<212> DNA
<213> adeno-associated virus, serotype 1

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<400> 202
atggctgccc atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtgg acttgaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctgtgtct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aaggggggag ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420
ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctctc gggcatcggc 480
aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgtgc tgtgggacct 600
actacaatgg cttcaggcgg tggcgacca atggcagaca ataacgaagg cgccgacgga 660
gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaata 780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag cccccctgg 840
gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

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atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960
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gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140
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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260
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atgatttttg gaaaagagag cgccggagct tcaaactctg cattggacaa tgtcatgatt 1680
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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800
gcattacctg gcatgggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860
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aagaacccgc ctctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980
gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040
gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100
tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccctg taccttaccg gtcccctgta a 2211

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<210> 203
<211> 2211
<212> DNA
<213> adeno-associated virus, serotype 6

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```

<400> 203
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60
gagtgggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180
aagggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaagaaga gggttctcga accttttggt ctggttgagg aaggtgctaa gacggctcct 420
ggaaaagaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480
aagacaggcc agcagcccg ctaaaagaga ctcaattttg gtcagactgg cgactcagag 540
tcagtccccg acccacaacc tctcggagaa cctccagcaa ccccgctgc tgtgggacct 600
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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcac 720
accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaadc 780
tccagtgcct caacgggggc cagcaacgac aaccactact tcggctacag caccctctgg 840
gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900
atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960
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gttcaagtct tctcggactc ggagtaccag ttgcccgtac tcctcggctc tgcgcaccag 1080
ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgagtagcgg ctacctaacg 1140
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tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260
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cagtacctgt attacctgaa cagaactcag aatcagtcgg gaagtgccca aaacaaggac 1380
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ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500
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ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcgggtgc 1620
atgatttttg gaaaggagag cgccggagct tcaaactctg cattggacaa tgtcatgatc 1680
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gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800
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gagttttcgg ctacaaagt tgccttcttc atcaccaggt attccacagg acaagtgagc 2040
gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100
tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160
tatactgagc ctgcgcccat tggcaccgtg tacctcaccg gtcccctgta a 2211

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<210> 204
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.63

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```

<400> 204
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agctcaaaacc tggcccacca ccaccaaaag ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180
aaggagagag cggatcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acagcggaga caaccctgac cccaagtaca accacgccga gcgagggttc 300
caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gcggagccag actctctctc gggaaccgga 480
aaagcggggc agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
aatacgatgg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggga cagagtcac 720
accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caagcagatt 780
tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggga aagactcatc 900
aacaacaatt ggggattccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960
aaggagggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacggtt 1020
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cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcttct 1260
cacagcagct acgcccacag ccagagttag gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagcggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctaggaactg gcttcttgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

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tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560  
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 atcttttgaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680  
 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800  
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 acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gcccattgg caccaggtag ctgactcgta atctgtaa 2208

&lt;210&gt; 205

&lt;211&gt; 2208

&lt;212&gt; DNA

&lt;213&gt; new AAV serotype, clone hu.56

&lt;400&gt; 205

atggctgccg atggttatct tccagattgg ctgaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttgtgct tcctggatac aagtacctcg gaccttcaa cggactcgac 180  
 aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca ggcctacgac 240  
 cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttcag 360  
 gcgaaaaaga ggggttctga acctctgggc ctggttgagg aacctgttaa gacggctccg 420  
 ggaaaaaaga ggccggtaga gactctcct gtggagccag actcctcctc gggaaaccga 480  
 aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540  
 tccgtacctg acccccagcc tctcggacag ccaccagcat cccctctggt tctgggaact 600  
 aatacagatg ctacaggcag tggcgacca atggcagaca ataacgaggg cgcgcagga 660  
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggca cagagtcgtc 720  
 accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt 780  
 tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840  
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 aacaacaact ggggattccg gcccaaaaga ctcaacttca agctgtttaa cattcaagtc 960  
 aaggaggtca cgcagaatga cggtagcag acgattgcca ataaccttac cagcacggtt 1020  
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 acttccaact acaacaaatc tgtaatatg gactttactg tggacactaa tgggggtgtat 2160  
 tcagagcctc gccctattgg caccagatac ctgactcgta atctgtaa 2208

<210> 206

<211> 2205

<212> DNA

<213> new AAV serotype, clone hu.57

<400> 206

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 agcaggggtc ttgtgcttcc tggatacaag tacctcggac cttcaacgg actcgacaag 180  
 ggagagccgg tcaacgaggg agacgccgcg gccctcggag acgacaaggc ctacgaccgg 240  
 cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc ggagtttcag 300  
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 aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga 420  
 aaaaagaggg ccgtagagca ctctcctgtg gagccagact cctcctcggg aaccggaaaa 480  
 gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc 540  
 gtacctgacc ccagcctctc cggacagcca ccagcagccc cctctggtct gggaaactaat 600  
 acgatggcta caggcagtg ggcaccaatg gcagacaata acgagggcgc cgacggagtg 660  
 ggtaattcct cgggagattg gcattgcgat tccacatgga tggcgacag agtcatcacc 720  
 accagacccc gcacctgggc cctgcccacc tacaacaacc acctctaca gcagatttcc 780  
 agccaatcag gagccagcaa tgacaaccac tactttggct acagcacccc ttgggggtat 840  
 tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag actcatcaac 900  
 aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat tcaagtcaag 960  
 gaggtcacgc agaattgacgg tacgacgacg attgccaata accttaccag cacggttcag 1020  
 gtgtttactg acttgagta ccagctcccg tacgtcctcg gctcggcgca tcaaggatgc 1080  
 ctccgcccgt tcccagcaga cgtcttcatt gtgccacagt atggatacct caccctgaac 1140  
 aacgggagtc agcggttagg acgtcttctc ttttactgcc tggagtactt tccttctcag 1200  
 atgcttcgta ccggaaacaa ctttaccttc agctacactt ttgaagacgt tcctttccac 1260  
 agcagctacg ctcacagtca aagtctggac cgtctcatga atcctctcat cgaccagtac 1320  
 ctgtattact tgagcagaac aaacactcca agcgggaacca ctacgcagtc caggcttcag 1380  
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 tggactggag ctaccaagta ccacctcaat ggcagagact ctctggtgaa tccgggcccg 1560  
 gccatggcca gccacaagga cgatgaagaa aagtttttct ctaaagcgg ggttctcatc 1620  
 tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggctcat gattacagac 1680  
 gaagaggaaa tcaggaccac caatcccgtg gctacggagc agtatgggtc tgtatctacc 1740  
 aacctccaga gcggcaacac acgagcagct acctcagatg tcaacacaca aggcgttctt 1800  
 ccaggcatgg tctggcagga cagagacgtg tacctgcagg ggcccatctg ggcaaaaatt 1860  
 ccacacacgg acggacattt tcacccctct cccctcatgg gcggatttgg acttaaacac 1920  
 cctcctccac agattctcat taagaatacc ccggtacctg cgaatccttc gaccaccttc 1980  
 agcgcggcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt cagcgtggag 2040  
 atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaat tcagtagact 2100

tccaactaca acaaatctgt taatgtggac' tttactgtgg acactaatgg ggtgtattca 2160  
gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 207  
<211> 2208  
<212> DNA  
<213> new AAV serotype, clone hu.58

<400> 207  
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60  
cagtgggtga agctcaaacc tggcccacca ccaccaaacg ccgcagagcg gcataaggac 120  
gacagcaggg gtcttgtgct tcttgggtac aagtacctcg gacccttcaa cggactcgac 180  
aagggagagc cggatcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240  
cggcagctcg acagcggaga caaccctgac ctcaagtacg accacgccga cgcggagttt 300  
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420  
ggaaaaaaga ggccggtaga gcaactctct gtggagccag actcctcctc gggaaaccgga 480  
aaagcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540  
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600  
aatacgtatg ctacaggcag tggcgacca atggcagaca ataacgatgg cgcgcagcga 660  
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720  
accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatt 780  
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840  
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900  
aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960  
agagaggtca cgcagaatga tggtagcagc acgattgcca ataaccttac cagcacgggt 1020  
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
tgcttcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140  
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta cttcccttct 1200  
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga tggtcctttc 1260  
cacagcagct acgtcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320  
tacctgtatt acttgagcag aacaaact ccaagcggaa ccaccacgca gtccaggctt 1380  
cagttttctc aggccggagc gagtgcatt cgggacagt ctaggaactg gcttcctgga 1440  
ccctgttacc gccagcagcg agtatcaaag acatctgcgg acaacaaca cagtgaatac 1500  
tcgtggattg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560  
ccggcaatgg ccagccacaa ggacgatgaa gaaaagtgtt ttctcagag cggggttctc 1620  
atctttggaa aacaaggatc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680  
gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740  
accaacctcc agagcggcaa cacacaagca tctactgcag atgtcaacac acaaggcggt 1800  
cttccaggca tggctctggc ggacagagac gtgtacctgc aggggcctat ctgggcaaag 1860  
attccgcaca cggacggaca ttttcacccc tctccctca tgggcggatt cggacttaaa 1920  
caccctctc cacagattct catcaaaaac accccggtac ctgcgaatcc ttcgaccacc 1980  
ttcagtgcgg caaagtgtgc ttccttcac acacagtatt ccacggggcg ggtcagcgtg 2040  
gagatcgagt gggagctaca gaaggagaac agcaaagcgt ggaatcccga gatccagtac 2100  
acttccaact acaaaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgat 2160  
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 208  
<211> 2208  
<212> DNA  
<213> new AAV serotype, clone hu.51

<400> 208  
 atggctgccg atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttggtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
 aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240  
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300  
 caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360  
 gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgtcaa gacggctcca 420  
 ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480  
 aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540  
 tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600  
 aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgcgcagcga 660  
 gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720  
 accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780  
 tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840  
 tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900  
 aacaacaact ggggatttcg acccaagaga ctcaacttca agtcttttaa cattcaagtc 960  
 aaagaggta cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacgggt 1020  
 cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080  
 tgctcccgcc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140  
 aacaacggga gtcaggcagt aggacgtctt tcatcttact gcctggagta ctttccttct 1200  
 cagatgctgc gtaccggaat caactttacc ttcagctaca cttttgagga cgttcctttc 1260  
 cacagcggct acgtcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320  
 tacctgtatt acttgagcac acaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380  
 cagttttctc aggcgggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440  
 ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500  
 tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560  
 ccggccatgg caagccacaa ggacaatgaa gaaaagtgtt ttcctcagag cggggttctc 1620  
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggc catgattaca 1680  
 gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct 1740  
 accaacctcc agagaggcaa cagacaagca gctaccgagc atgtcaacac acaaggcggt 1800  
 cttccaggca tgggtctggc ggacagagat gtgtaccttc aggggcccac ctgggcaaag 1860  
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 caccctcttc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980  
 ttcagtgcgg caaagtgtgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040  
 gagatcgagt gggagctgca gaaggaaaac agcaaagcgt ggaatcccga aattcagtac 2100  
 acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160  
 tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 209  
 <211> 2208  
 <212> DNA  
 <213> new AAV serotype, clone hu.49

<400> 209  
 atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga 60  
 cagtgggtgga agctcaaacc tggcccacca ccaccaaaagc ccgcagagcg gcataaggac 120  
 gacagcaggg gtcttggtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180  
 aaggagagc cggtaacga ggcagacgcc gcggccctcg agtacgacaa ggcctacgac 240  
 cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300

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caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga ggggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gtggagccag actcctcctc gggaacagga 480
aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg ctacaggcag tggcgacca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc 780
tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaggagggtca cgcagaatga cggtagcagc acgattgcc aataacctac cagcacgggt 1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga 1080
tgctctccgc cgctccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140
aacaacggga gtcaggcagt aggacgtctc tcattttact gcctggagta ctttcttct 1200
cagatgcttc gtaccggaaa caactttacc ttcagctaca ctttgagga tgctcttct 1260
cacagcagct acgttcacag ccagagtgtg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380
cagttttctc aggccggagc aagtgcatt cgggaccagt ctaggaactg gcttcttga 1440
ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg ccagccacaa ggacgatgaa gaaaagtgtt ttcctcaaag cgggggtctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740
accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt 1800
cttcaggca tggctctgga ggacagagac gtgcacctgc aggggcctat ctgggcaaag 1860
attccacaca cggacggaca ttttccccc tctcccctca tgggcggatt tggacttaa 1920
caccctctc cacagattct catcaagaac accccgtac ctgcaaatcc ttcgaccacc 1980
ttcagtgcgg caaagtgtgc ttccttcatc acacagtatt ccacagggca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggagaac agcaaacgtt ggaaccccg gatccagtac 2100
acttccaact acaacaatc tgtaatgtg gactttactg tggacactaa tgggtgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 210
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.52

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<400> 210
atggctgccc atggttatct tccagattgg ctccaggaca ctctctctga aggaataaga 60
cagtgggtga agtcaaacc tggccacca ccaccaaagc ccgacagagc gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctgc gacccttcaa cggactcgac 180
aaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctct gtggagccag actcctcctc gggaaccgga 480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600

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aatac gatg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa tcggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta cagacaaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggatttcg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggcca cgcagaatga cggtagcagc acgattgccataaaccttac cagcacggtt 1020
cagggtgtta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cggtcccagc agacgtcttc atgggtgccac agtatggata cctcaccctg 1140
agcaacggga gtcaggcagt aggacgtctt tcatcttact gcccgagga ctttccttct 1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcac aacaaacct ccaagtggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cgggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcggt 1800
cttcaggga tggcttgga ggacagagat gtgtaccttc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctccctca tgggtggatt cggacctaaa 1920
cacctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatccga aattcagtac 2100
acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gcccattgg caccagatac ctgactcgta atttgtaa 2208

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<210> 211
<211> 2208
<212> DNA
<213> adeno-associated virus, serotype 2

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<400> 211
atggctgccc atgggtatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agctcaaac tggcccacca ccaccaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttggtgct tcctgggtac aagtacctcg gaccttcaa cggactcgac 180
aaggagagc cggtaacga ggcagacgcc gcggccctcg agcacgaca agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctgg tctgggaact 600
aatac gatg ctacaggcag tggcgaccca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

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aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagagggtca cgcagaatga cggtagacg acgattgccataaaccttac cagcacgggt 1020
cagggtgttta ctgactcggga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct 1200
cagatgtctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaacact ccaagtggaa ccaccacgca gtcaaggcct 1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaactg gcttccttga 1440
ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
tcgtggactg gagctacaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc agagaggcaa cagacaagca gctaccgag atgtcaacac acaaggcgtt 1800
cttcaggca tggctcggca ggacagagat gtgtacctc agggggccat ctgggcaaag 1860
attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920
caccctctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980
ttcagtgcgg caaagtttgc ttccttcac acacagtact ccacgggaca ggtcagcgtg 2040
gagatcgagt gggagctgca gaaggaaaac agcaaagct ggaatcccga aattcagtac 2100
acttccaact acaacaagtc tgtaaatgtg gactttactg tggacactaa tggcgtgtat 2160
tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

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<210> 212
<211> 2208
<212> DNA
<213> new AAV serotype, clone hu.64

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<400> 212
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtgga agtcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtctgtgtct tcctgggtac aagtacctg gacccttcaa cggactcgac 180
aaggagagc cggtaacga ggacagcgc gcggccctcg agcacgacaa ggcctacgac 240
cggcagctcg acggcggaga caaccgtac ctcaagtaca accacgccga cgcggagtct 300
caggagcgtc ttaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctctt gcggagccag actcctctc ggaaccgga 480
aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac 540
tccgtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact 600
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tccagccaat caggagctc aaacgacaac cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt cactgccac ttttcgccac gtgactggca aagactcatc 900
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tgcttcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
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 gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740  
 accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800  
 cttccaggca tgggtgtggc ggacagagac gtgtacctgc aggggcccac ctgggcaaaag 1860  
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 caccctcccc cgagattct catcaagaac accccggtag ctgcgaatcc ttcgactacc 1980  
 ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040  
 gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtag 2100  
 acttccaact acaacaaatc tgtaaatgtg gactttactg tggacactaa tgggtgtgtat 2160  
 tcagagcctc gccccattgg caccagatag ctgactcgta atctgtaa 2208

<210> 213  
 <211> 2214  
 <212> DNA  
 <213> adeno-associated virus, serotype 7

<400> 213  
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 gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120  
 aacggccggg gtctggtgct tcttggttac aagtacctcg gaccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca ggcggcctcg agcacgaca ggcttacgac 240  
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cggcgagttt 300  
 caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360  
 gccagaagc gggttctcga acctctcggg ctggttgagg aaggcgctaa gacggctcct 420  
 gcaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcattc 480  
 ggcaagaag gccagcagcc cgccagaag agactcaatt tcggtcagac tggcgactca 540  
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 tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660  
 ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
 attaccacca gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa 780  
 atctccagtg aaactgcagg tagtaccac gacaacacct acttcggcta cagcaccctc 840  
 tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900  
 ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960  
 caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020  
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 gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat 1380  
 cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg 1440  
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 cttaaacatc cgctcctca gatcctgac aagaacactc ccgttcccgc taatcctccg 1980  
 gaggtgttta ctctgccaa gtttgcttcg ttcacacac agtacagcac cggacaagtc 2040  
 agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgtggaa cccggagatt 2100  
 cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt 2160  
 gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct gtaa 2214

<210> 214  
 <211> 2217  
 <212> DNA  
 <213> adeno-associated virus, serotype 8

<400> 214  
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 gacggccggg gtctgggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180  
 aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240  
 cagcagctgc aggcgggtga caatccgtac ctgcgtata accacgccga cgccgagttt 300  
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 gccaaagaag gggttctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct 420  
 ggaaagaaga gaccggtaga gccatcacc cagcgttctc cagactctc tacgggcatc 480  
 ggcaagaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540  
 gagtcagttc cagaccctca acctctcggg gaacctccag cagcgcctc tgggtgtgga 600  
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 ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
 atcaccacca gcaccgaac ctggggcctg cccacctaca acaaccacct ctacaagcaa 780  
 atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840  
 ccttgggggt attttgactt taacagattc cactgccact ttaccacag tgactggcag 900  
 cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960  
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 ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200  
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cagggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggccccatc 1860  
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 ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040  
 gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgtg gaaccccgag 2100  
 atccagtaca cttccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160  
 ggcgtgtact ctgaaccccg cccattggc acccgttacc tcaccgtaa tctgtaa 2217

<210> 215  
 <211> 2217  
 <212> DNA  
 <213> new AAV serotype, clone hu.67

<400> 215  
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 gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120  
 gacggccggg gtctggtgct tcttggtac aagtacctg gacccttcaa cggactcgac 180  
 aagggggagc ccgtcaatgc ggcggacgca gcgccctcg agcacgacaa ggcctacgac 240  
 cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300  
 caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttcag 360  
 gccaagaagc gggttctcga acctctcggg ctggttgagg aagctgctaa gacggctcct 420  
 ggaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480  
 ggcaagaaag gccagcagcc cgtaaaaaag agactgaact ttggtcagac tggcgactca 540  
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 ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720  
 atcaccacca gacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780  
 atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840  
 ccctgggggt attttgactt caacagattc cactgccact tctcaccag tgactggcag 900  
 cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960  
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 caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140  
 cttactactga acaatggaag tcaagccgta ggccgttcct cttctactg cctggaatat 1200  
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attcagtaca cttcaaacta ctacaaatct acaaattgtgg actttgctgt caatacagag 2160  
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<210> 216  
 <211> 724  
 <212> PRT  
 <213> vp1, serotype 5

<400> 216

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu  
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 Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys  
 20 25 30  
 Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly  
 35 40 45  
 Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val  
 50 55 60  
 Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu  
 65 70 75 80  
 Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
 85 90 95  
 Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn  
 100 105 110  
 Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe  
 115 120 125  
 Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile  
 130 135 140  
 Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser  
 145 150 155 160  
 Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln  
 165 170 175  
 Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr  
 180 185 190  
 Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala  
 195 200 205  
 Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp  
 210 215 220  
 Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro  
 225 230 235 240  
 Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp  
 245 250 255  
 Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
 260 265 270  
 Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln  
 275 280 285  
 Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val  
 290 295 300  
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr  
 305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp  
 325 330 335  
 Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys  
 340 345 350  
 Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr  
 355 360 365  
 Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser  
 370 375 380  
 Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn  
 385 390 395 400  
 Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser  
 405 410 415  
 Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp  
 420 425 430  
 Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln  
 435 440 445  
 Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp  
 450 455 460  
 Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly  
 465 470 475 480  
 Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu  
 485 490 495  
 Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr  
 500 505 510  
 Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile  
 515 520 525  
 Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu  
 530 535 540  
 Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg  
 545 550 555 560  
 Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser  
 565 570 575  
 Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro  
 580 585 590  
 Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
 595 600 605  
 Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met  
 610 615 620  
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn  
 625 630 635 640  
 Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser  
 645 650 655  
 Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu  
 660 665 670  
 Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln

675

680

685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp  
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu  
705 710 715 720

Thr Arg Pro Leu

<210> 217

<211> 736

<212> PRT

<213> vp1, serotype 3-3

<400> 217

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro  
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly  
130 135 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly  
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His

275                      280                      285  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290                      295                      300  
 Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val  
 305                      310                      315                      320  
 Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325                      330                      335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340                      345                      350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355                      360                      365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370                      375                      380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385                      390                      395                      400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405                      410                      415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420                      425                      430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr  
 435                      440                      445  
 Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser  
 450                      455                      460  
 Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro  
 465                      470                      475                      480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn  
 485                      490                      495  
 Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn  
 500                      505                      510  
 Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys  
 515                      520                      525  
 Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly  
 530                      535                      540  
 Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile  
 545                      550                      555                      560  
 Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln  
 565                      570                      575  
 Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr  
 580                      585                      590  
 Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln  
 595                      600                      605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610                      615                      620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625                      630                      635                      640



Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val  
 705 710 715 720  
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
 <210> 218  
 <211> 734  
 <212> PRT  
 <213> vp1, serotype 4-4  
 <400> 218  
 Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu  
 1 5 10 15  
 Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys  
 20 25 30  
 Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly  
 35 40 45  
 Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val  
 50 55 60  
 Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln  
 65 70 75 80  
 Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp  
 85 90 95  
 Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn  
 100 105 110  
 Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu  
 115 120 125  
 Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro  
 130 135 140  
 Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys  
 145 150 155 160  
 Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr  
 165 170 175  
 Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser  
 180 185 190  
 Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly  
 195 200 205  
 Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys  
 210 215 220  
 Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr  
 225 230 235 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu  
 245 250 255  
 Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr  
 260 265 270  
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln  
 275 280 285  
 Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val  
 290 295 300  
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu  
 305 310 315 320  
 Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp  
 325 330 335  
 Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser  
 340 345 350  
 Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr  
 355 360 365  
 Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn  
 370 375 380  
 Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly  
 385 390 395 400  
 Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser  
 405 410 415  
 Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile  
 420 425 430  
 Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu  
 435 440 445  
 Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn  
 450 455 460  
 Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln  
 465 470 475 480  
 Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr  
 485 490 495  
 Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly  
 500 505 510  
 Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro  
 515 520 525  
 Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys  
 530 535 540  
 Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser  
 545 550 555 560  
 Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly  
 565 570 575  
 Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp  
 580 585 590  
 Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg  
 595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp  
 610 615 620  
 Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His  
 625 630 640  
 Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro  
 645 650 655  
 Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr  
 660 665 670  
 Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu  
 675 680 685  
 Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly  
 690 695 700  
 Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr  
 705 710 715 720  
 Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu  
 725 730

<210> 219  
 <211> 736  
 <212> PRT  
 <213> vp1, serotype 1

<400> 219

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380  
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 220  
 <211> 736  
 <212> PRT  
 <213> vp1, serotype 6

<400> 220

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380  
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly

530                      535                      540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545                      550                      555                      560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565                      570                      575  
 Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala  
 580                      585                      590  
 Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595                      600                      605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610                      615                      620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625                      630                      635                      640  
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645                      650                      655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660                      665                      670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675                      680                      685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690                      695                      700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705                      710                      715                      720  
 Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725                      730                      735  
  
 <210> 221  
 <211> 735  
 <212> PRT  
 <213> vp1, serotype 2  
  
 <400> 221  
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1                      5                      10                      15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20                      25                      30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35                      40                      45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50                      55                      60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65                      70                      75                      80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85                      90                      95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100                      105                      110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115                      120                      125  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

130	135	140
Pro Val Glu His Ser 145	Pro Val Glu Pro Asp 150	Ser Ser Ser Gly Thr Gly 155 160
Lys Ala Gly Gln Gln 165	Pro Ala Arg Lys Arg 170	Leu Asn Phe Gly Gln Thr 175
Gly Asp Ala Asp 180	Ser Val Pro Asp Pro 185	Gln Pro Leu Gly Gln Pro Pro 190
Ala Ala Pro 195	Ser Gly Leu Gly Thr 200	Asn Thr Met Ala Thr Gly Ser Gly 205
Ala Pro Met Ala Asp Asn 210	Asn 215	Glu Gly Ala Asp Gly Val Gly Asn Ser 220
Ser Gly Asn Trp His 225	Cys 230	Asp Ser Thr Trp Met Gly Asp Arg Val Ile 235 240
Thr Thr Ser Thr 245	Arg Thr Trp Ala Leu Pro 250	Thr Tyr Asn Asn His Leu 255
Tyr Lys Gln Ile 260	Ser Ser Gln Ser Gly 265	Ala Ser Asn Asp Asn His Tyr 270
Phe Gly Tyr 275	Ser Thr Pro Trp Gly 280	Tyr Phe Asp Phe Asn Arg Phe His 285
Cys His Phe Ser Pro Arg 290	Asp 295	Trp Gln Arg Leu Ile Asn Asn Asn Trp 300
Gly Phe Arg Pro Lys 305	Arg 310	Leu Asn Phe Lys Leu Phe Asn Ile Gln Val 315 320
Lys Glu Val Thr 325	Gln Asn Asp Gly Thr Thr 330	Thr Ile Ala Asn Asn Leu 335
Thr Ser Thr 340	Val Gln Val Phe Thr 345	Asp Ser Glu Tyr Gln Leu Pro Tyr 350
Val Leu Gly 355	Ser Ala His Gln Gly 360	Cys Leu Pro Pro Phe Pro Ala Asp 365
Val Phe Met Val Pro Gln 370	Tyr 375	Gly Tyr Leu Thr Leu Asn Asn Gly Ser 380
Gln Ala Val Gly Arg 385	Ser 390	Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser 395 400
Gln Met Leu Arg 405	Thr Gly Asn Asn Phe 410	Thr Phe Ser Tyr Thr Phe Glu 415
Asp Val Pro Phe His 420	Ser Ser Tyr Ala 425	His Ser Gln Ser Leu Asp Arg 430
Leu Met Asn Pro Leu Ile 435	Asp Gln Tyr Leu Tyr Tyr 440	Leu Ser Arg Thr 445
Asn Thr Pro Ser Gly Thr 450	Thr Thr Thr Gln Ser Arg 455	Leu Gln Phe Ser Gln 460
Ala Gly Ala Ser Asp 465	Ile 470	Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly 475 480
Pro Cys Tyr Arg Gln 485	Gln Arg Val Ser Lys 490	Thr Ser Ala Asp Asn Asn 495



Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 222  
 <211> 737  
 <212> PRT  
 <213> vp1, serotype 7

<400> 222

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp  
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
515 520 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
530 535 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu  
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
565 570 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
625 630 635 640

Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
725 730 735

Leu

<210> 223  
<211> 738  
<212> PRT  
<213> vp1, serotype 8

<400> 223

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr  
 405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly  
 450 455 460  
 Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile  
 530 535 540  
 Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735  
 Asn Leu

<210> 224  
 <211> 736  
 <212> PRT  
 <213> vp1, modified hu.46

&lt;400&gt; 224

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 20 25 30  
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160  
 Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175  
 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190  
 Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255  
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270  
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285  
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300  
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320  
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335  
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350  
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala

355 360 365  
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380  
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400  
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415  
 Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp  
 420 425 430  
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445  
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser  
 450 455 460  
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510  
 Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540  
 Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575  
 Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590  
 Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605  
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620  
 Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 225  
 <211> 735  
 <212> PRT  
 <213> vp1, modified hu.29

<400> 225

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
 145 150 155 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320



Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
 435 440 445  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr  
 580 585 590  
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

<210> 226  
<211> 735  
<212> PRT  
<213> vp1, modified hu.7

<400> 226

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly  
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
 290 295 300  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr  
 435 440 445  
 Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly  
 500 505 510  
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr  
 580 585 590  
 Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln  
 660 665 670  
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
 675 680 685  
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
 690 695 700  
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr  
 705 710 715 720  
 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735

<210> 227  
 <211> 728  
 <212> PRT  
 <213> vp1, modified cy.5

<400> 227

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln  
 145 150 155 160  
 Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu  
 165 170 175  
 Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser  
 180 185 190  
 Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala  
 195 200 205  
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp  
 210 215 220  
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr  
 225 230 235 240  
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile  
 245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser  
 260 265 270  
 Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser  
 275 280 285  
 Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro  
 290 295 300  
 Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr  
 305 310 315 320  
 Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile  
 325 330 335  
 Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser  
 340 345 350  
 Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile  
 355 360 365  
 Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly  
 370 375 380  
 Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg  
 385 390 395 400  
 Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe  
 405 410 415  
 His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro  
 420 425 430  
 Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr  
 435 440 445  
 Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met  
 450 455 460  
 Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln  
 465 470 475 480  
 Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp  
 485 490 495  
 Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn  
 500 505 510  
 Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe  
 515 520 525  
 Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys  
 530 535 540  
 Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr  
 545 550 555 560  
 Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu  
 565 570 575  
 Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly  
 580 585 590  
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
 595 600 605  
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
 Page 345

610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro  
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser  
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn  
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu  
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly  
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu  
725

<210> 228  
 <211> 728  
 <212> PRT  
 <213> vp1, modified rh.13

<400> 228

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln  
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu  
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser  
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala  
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp

210	215	220
His Cys Asp Ser Thr Trp 225 230	Leu Gly Asp Arg Val 235	Ile Thr Thr Ser Thr 240
Arg Thr Trp Ala Leu 245	Pro Thr Tyr Asn Asn 250	His Leu Tyr Lys Gln Ile 255
Ser Ser Gln Ser Gly Ala Thr Asn 260 265	Asp Asn His Phe Phe Gly 270	Tyr Ser
Thr Pro Trp Gly Tyr Phe Asp 275 280	Phe Asn Arg Phe His Cys 285	His Phe Ser
Pro Arg Asp Trp Gln Arg Leu 290 295	Ile Asn Asn Asn Trp 300	Gly Phe Arg Pro
Arg Lys Leu Arg Phe Lys 305 310	Leu Phe Asn Ile Gln Val 315	Lys Glu Val Thr 320
Thr Asn Asp Gly Val 325	Thr Thr Ile Ala Asn 330	Asn Leu Thr Ser Thr Ile 335
Gln Val Phe Ser 340	Asp Ser Glu Tyr Gln 345	Leu Pro Tyr Val Leu Gly Ser 350
Ala His Gln Gly Cys Leu Pro 355 360	Pro Phe Pro Ala Asp Val 365	Phe Met Ile
Pro Gln Tyr Gly Tyr Leu Thr 370 375	Leu Asn Asn Gly Ser 380	Gln Ser Val Gly
Arg Ser Ser Phe Tyr Cys 385 390	Leu Glu Tyr Phe Pro 395	Ser Gln Met Leu Arg 400
Thr Gly Asn Asn Phe 405	Glu Phe Ser Tyr Thr 410	Phe Glu Glu Val Pro Phe 415
His Ser Ser Tyr Ala His Ser 420 425	Gln Ser Leu Asp Arg Leu 430	Met Asn Pro
Leu Ile Asp Gln Tyr Leu Tyr 435 440	Tyr Leu Ala Arg Thr Gln 445	Ser Thr Thr
Gly Ser Thr Arg Glu Leu 450 455	Gln Phe His Gln Ala Gly 460	Pro Asn Thr Met
Ala Glu Gln Ser Lys Asn 465 470	Trp Leu Pro Gly Pro 475	Cys Tyr Arg Gln Gln 480
Arg Leu Ser Lys Asn 485	Ile Asp Ser Asn Asn 490	Ser Asn Phe Ala Trp 495
Thr Gly Ala Thr Lys Tyr His 500 505	Leu Asn Gly Arg Asn Ser 510	Leu Thr Asn
Pro Gly Val Ala Met Ala Thr 515 520	Asn Lys Asp Asp Glu Asp 525	Gln Phe Phe
Pro Ile Asn Gly Val Leu Val 530 535	Phe Gly Lys Thr Gly 540	Ala Ala Asn Lys
Thr Thr Leu Glu Asn Val 545 550	Leu Met Thr Ser Glu 555	Glu Glu Ile Lys Thr 560
Thr Asn Pro Val Ala 565	Thr Glu Glu Tyr Gly 570	Val Val Ser Ser Asn Leu 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly  
 580 585 590  
 Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
 595 600 605  
 Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
 610 615 620  
 Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
 625 630 635 640  
 Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro  
 645 650 655  
 Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser  
 660 665 670  
 Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn  
 675 680 685  
 Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu  
 690 695 700  
 Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly  
 705 710 715 720  
 Thr Arg Tyr Leu Thr Arg Asn Leu  
 725

<210> 229  
 <211> 729  
 <212> PRT  
 <213> vp1, modified rh.37

<400> 229

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln  
 145 150 155 160  
 Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu  
 165 170 175



Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser  
 180 185 190  
 Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala  
 195 200 205  
 Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp  
 210 215 220  
 His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr  
 225 230 235 240  
 Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile  
 245 250 255  
 Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr  
 260 265 270  
 Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe  
 275 280 285  
 Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg  
 290 295 300  
 Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val  
 305 310 315 320  
 Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr  
 325 330 335  
 Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly  
 340 345 350  
 Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met  
 355 360 365  
 Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val  
 370 375 380  
 Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu  
 385 390 395 400  
 Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro  
 405 410 415  
 Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn  
 420 425 430  
 Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr  
 435 440 445  
 Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr  
 450 455 460  
 Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln  
 465 470 475 480  
 Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala  
 485 490 495  
 Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr  
 500 505 510  
 Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe  
 515 520 525  
 Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn  
 530 535 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys  
 545 550 555 560  
 Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn  
 565 570 575  
 Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln  
 580 585 590  
 Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln  
 595 600 605  
 Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro  
 610 615 620  
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile  
 625 630 635 640  
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr  
 645 650 655  
 Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val  
 660 665 670  
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp  
 675 680 685  
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val  
 690 695 700  
 Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile  
 705 710 715 720  
 Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725

<210> 230  
 <211> 737  
 <212> PRT  
 <213> vp1, modified rh.67

<400> 230

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220  
 Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn  
 260 265 270  
 Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala  
 435 440 445  
 Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln  
 450 455 460  
 Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile  
 530 535 540  
 Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu  
 545 550 555 560  
 Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala  
 580 585 590  
 Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605  
 Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620  
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640  
 Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655  
 Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile  
 660 665 670  
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685  
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser  
 690 695 700  
 Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly  
 705 710 715 720  
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn  
 725 730 735

Leu

<210> 231  
 <211> 738  
 <212> PRT  
 <213> vpl, modified rh.2

<400> 231

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15  
 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu

450                      455                      460  
 Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp  
 465                      470                      475                      480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
                     485                      490                      495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
                     500                      505                      510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
                     515                      520                      525  
 His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met  
                     530                      535                      540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val  
 545                      550                      555                      560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
                     565                      570                      575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala  
                     580                      585                      590  
 Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
                     595                      600                      605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
                     610                      615                      620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625                      630                      635                      640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
                     645                      650                      655  
 Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe  
                     660                      665                      670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
                     675                      680                      685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
                     690                      695                      700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705                      710                      715                      720  
 Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
                     725                      730                      735  
 Asn Leu

<210> 232  
 <211> 738  
 <212> PRT  
 <213> vp1, modified rh.58

<400> 232

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1                      5                      10                      15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20                      25                      30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro

35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
 210 215 220  
 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
 260 265 270  
 Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
 275 280 285  
 Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
 290 295 300  
 Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
 305 310 315 320  
 Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
 325 330 335  
 Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
 340 345 350  
 Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720  
 Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
 725 730 735

Asn Leu

<210> 233  
 <211> 738  
 <212> PRT



&lt;213&gt; vpl, modified rh.64

&lt;400&gt; 233

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
1 5 10 15Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
145 150 155 160Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln  
165 170 175Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
180 185 190Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly  
195 200 205Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser  
210 215 220Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
225 230 235 240Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
245 250 255Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp  
260 265 270Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn  
275 280 285Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn  
290 295 300Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn  
305 310 315 320Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala  
325 330 335Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln  
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe  
 355 360 365  
 Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn  
 370 375 380  
 Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr  
 385 390 395 400  
 Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr  
 405 410 415  
 Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser  
 420 425 430  
 Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu  
 435 440 445  
 Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu  
 450 455 460  
 Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp  
 465 470 475 480  
 Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser  
 485 490 495  
 Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His  
 500 505 510  
 Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr  
 515 520 525  
 Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met  
 530 535 540  
 Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val  
 545 550 555 560  
 Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr  
 565 570 575  
 Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala  
 580 585 590  
 Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val  
 595 600 605  
 Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile  
 610 615 620  
 Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe  
 625 630 635 640  
 Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val  
 645 650 655  
 Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe  
 660 665 670  
 Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu  
 675 680 685  
 Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr  
 690 695 700  
 Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu  
 705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg  
725 730 735

Asn Leu

<210> 234  
<211> 735  
<212> PRT  
<213> vp1, modified ch.5

<400> 234

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr  
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
 305 310 315 320  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
 325 330 335  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
 340 345 350  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
 355 360 365  
 Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
 370 375 380  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
 385 390 395 400  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
 405 410 415  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
 420 425 430  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr  
 435 440 445  
 Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln  
 450 455 460  
 Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly  
 465 470 475 480  
 Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn  
 485 490 495  
 Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly  
 500 505 510  
 Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp  
 515 520 525  
 Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys  
 530 535 540  
 Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr  
 545 550 555 560  
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr  
 565 570 575  
 Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr  
 580 585 590  
 Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp  
 595 600 605  
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 610 615 620  
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 625 630 635 640  
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn  
 645 650 655  
 Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln

000

000

670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys  
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr  
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr  
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
725 730 735

&lt;210&gt; 235

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; vp1, modified rh.8

&lt;400&gt; 235

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly  
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn

260 265 270  
 Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val  
 435 440 445  
 Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser  
 450 455 460  
 Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro  
 465 470 475 480  
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn  
 485 490 495  
 Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn  
 500 505 510  
 Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys  
 515 520 525  
 Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly  
 530 535 540  
 Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile  
 545 550 555 560  
 Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu  
 565 570 575  
 Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln  
 580 585 590  
 Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln  
 595 600 605  
 Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640  
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655  
 Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr  
 660 665 670  
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685  
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn  
 690 695 700  
 Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val  
 705 710 715 720  
 Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu  
 725 730 735  
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 <211> 737  
 <212> PRT  
 <213> vp1, modified hu.43  
 <400> 236  
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 Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30  
 Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60  
 Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80  
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala  
 85 90 95  
 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125  
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140  
 Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile  
 145 150 155 160  
 Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln  
 165 170 175  
 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro  
 180 185 190  
 Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly  
 195 200 205  
 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn  
 210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val  
 225 230 235 240  
 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His  
 245 250 255  
 Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn  
 260 265 270  
 His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg  
 275 280 285  
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn  
 290 295 300  
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile  
 305 310 315 320  
 Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn  
 325 330 335  
 Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu  
 340 345 350  
 Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro  
 355 360 365  
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn  
 370 375 380  
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe  
 385 390 395 400  
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr  
 405 410 415  
 Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu  
 420 425 430  
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn  
 435 440 445  
 Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe  
 450 455 460  
 Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu  
 465 470 475 480  
 Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp  
 485 490 495  
 Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu  
 500 505 510  
 Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His  
 515 520 525  
 Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe  
 530 535 540  
 Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met  
 545 550 555 560  
 Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu  
 565 570 575  
 Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro  
 580 585 590



Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp  
 595 600 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro  
 610 615 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly  
 625 630 635 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro  
 645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile  
 660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu  
 675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser  
 690 695 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly  
 705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro  
 725 730 735

Leu